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PATENT & SEQUENCE LISTING

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Martin, Denis
Charland, Nathalie
Ouellet, Catherine

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aaatctggaa gaaaatatga gtgttctagc agaagaatta aagtaggaa agaatgaaaa	120
tcaataaaaa atatctagca gggtcagtg cagtccttgc cctaagtgtt tgttcctatg	180

aacttggtcg tcaccaagct ggtcagggtta agaaagagtc taatcgagtt tcttatatag	240
atggtgatca ggctggtcaa aaggcagaaa atttgacacc agatgaagtc agtaagagag	300
aggggatcaa cgccgaacaa attgttatca agattacgga tcaaggttat gtgacctctc	360
atggagacca ttatcattac tataatggca aggttcctta tgatgccatc atcagtgaag	420
aactttctcat gaaagatccg aattatcagt tgaaggattc agacattgtc aatgaaatca	480
aggggtggcta tgtgattaag gtagacggaa aatactatgt ttaccttaaa gatgcgggccc	540
atgcggacaa tattcggaca aaagaagaga ttaaactgca gaagcaggaa cacagtcata	600
atcataactc aagagcagat aatgctgttg ctgcagccag agcccaagga cgttatacaa	660
cggatgatgg gtatatcttc aatgcatctg atatcattga ggacacgggt gatgcttata	720
tcgttctca cggcgaccat taccattaca ttccctaagaa tgagttatca gctagcgagt	780
tagctgctgc agaagcctat tggaatggga agcagggatc tcgtccttct tcaagttcta	840
gttataatgc aaatccagtt caaccaagat tgtcagagaa ccacaatctg actgtcactc	900
caacttatca tcaaaatcaa ggggaaaaca tttcaagcct ttacagtga ttgtatgcta	960
aacccttattc agaacgcat gtagaatctg atggccttat ttctgaccca gcgcaaatca	1020
caagtccaac cgccagaggt gtagctgtcc ctcatggtaa ccattaccac ttatccctt	1080
atgaacaaat gtctgaattg gaaaaacgaa ttgctcgat tattccctt cgttatcggt	1140
caaaccattg ggtaccagat tcaagaccag aacaaccaag tccacaatcg actccggaac	1200
ctagtccaag tctgcaacct gcaccaaact ctcaaccagc tccaagcaat ccaattgatg	1260
agaaattggt caaagaagct gtctgaaaag taggcgatgg ttatgtcttt gaggagaatg	1320
gagtttctcg ttatatccca gccaggatc ttctcagcaga aacagcagca ggcattgata	1380
gcaaactggc caagcaggaa agtttatctc ataagctagg agctaagaaa actgacctcc	1440
catctagtga tcgagaattt tacaataagg cttatgactt actagcaaga attcaccaag	1500
atttacttga taataaaggc cgacaagttg attttgaggt ttgggataac ctggttgaac	1560
gactcaagga tgtctcaagt gataaagtca agttagtggg tgatattctt gccttcttag	1620
ctccgattcg tcatccagaa cgtttaggaa aaccaaagtc gcaaattacc tacactgatg	1680
atgagattca agtagccaag ttggcaggca agtacacaac agaagacggt tatatctttg	1740
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gccactggat taaaaaagat agtttgtctg aagctgagag agcggcagcc caggcttatg	1860
ctaaagagaa aggtttgacc cctccttcga cagaccacca ggattcagga aatactgagg	1920

caaaaggagc agaagctatc tacaaccgcg tgaaagcagc taagaagggtg ccacttgatc 1980
 gtatgcctta caatcttcaa tatactgtag aagtcaaaaa cggtagttaa atcatacctc 2040
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 ctaaggggta tagtcttgag gatcttttgg cgactgtcaa gtactatgtc gaacatccaa 2160
 acgaacgtcc gcattcagat aatgggtttg gtaacgctag tgaccatgtt cgtaaaaata 2220
 aggcagacca agatagtaaa cctgatgaag ataaggaaca tgatgaagta agtgagccaa 2280
 ctcaccctga atctgatgaa aaagagaatc acgctgggtt aaatccttca gcagataatc 2340
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 aggctgaaat tcctcaagta gagaattctg ttattaacgc taagatagca gatgcggagg 2460
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 gtctaaaaag tagtcttctt ctcggaacga aagataataa cactatttca gcagaagtag 2580
 atagtctctt ggctttgtta aaagaaagtc aaccggctcc tatacagtag taaaatgaa 2639

<210> 6
 <211> 1039
 <212> PRT
 <213> Streptococcus pneumoniae

<400> 6

Met Lys Phe Ser Lys Lys Tyr Ile Ala Ala Gly Ser Ala Val Ile Val
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Ser Leu Ser Leu Cys Ala Tyr Ala Leu Asn Gln His Arg Ser Gln Glu
 20 25 30

Asn Lys Asp Asn Asn Arg Val Ser Tyr Val Asp Gly Ser Gln Ser Ser
 35 40 45

Gln Lys Ser Glu Asn Leu Thr Pro Asp Gln Val Ser Gln Lys Glu Gly
 50 55 60

Ile Gln Ala Glu Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val
 65 70 75 80

Thr Ser His Gly Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr
 85 90 95

Asp Ala Leu Phe Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln
100 105 110

Leu Lys Asp Ala Asp Ile Val Asn Glu Val Lys Gly Gly Tyr Ile Ile
115 120 125

Lys Val Asp Gly Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala
130 135 140

Asp Asn Val Arg Thr Lys Asp Glu Ile Asn Arg Gln Lys Gln Glu His
145 150 155 160

Val Lys Asp Asn Glu Lys Val Asn Ser Asn Val Ala Val Ala Arg Ser
165 170 175

Gln Gly Arg Tyr Thr Thr Asn Asp Gly Tyr Val Phe Asn Pro Ala Asp
180 185 190

Ile Ile Glu Asp Thr Gly Asn Ala Tyr Ile Val Pro His Gly Gly His
195 200 205

Tyr His Tyr Ile Pro Lys Ser Asp Leu Ser Ala Ser Glu Leu Ala Ala
210 215 220

Ala Lys Ala His Leu Ala Gly Lys Asn Met Gln Pro Ser Gln Leu Ser
225 230 235 240

Tyr Ser Ser Thr Ala Ser Asp Asn Asn Thr Gln Ser Val Ala Lys Gly
245 250 255

Ser Thr Ser Lys Pro Ala Asn Lys Ser Glu Asn Leu Gln Ser Leu Leu
260 265 270

Lys Glu Leu Tyr Asp Ser Pro Ser Ala Gln Arg Tyr Ser Glu Ser Asp
275 280 285

Gly Leu Val Phe Asp Pro Ala Lys Ile Ile Ser Arg Thr Pro Asn Gly
290 295 300

Val Ala Ile Pro His Gly Asp His Tyr His Phe Ile Pro Tyr Ser Lys
305 310 315 320

Leu Ser Ala Leu Glu Glu Lys Ile Ala Arg Met Val Pro Ile Ser Gly

325

330

335

Thr Gly Ser Thr Val Ser Thr Asn Ala Lys Pro Asn Glu Val Val Ser
 340 345 350

Ser Leu Gly Ser Leu Ser Ser Asn Pro Ser Ser Leu Thr Thr Ser Lys
 355 360 365

Glu Leu Ser Ser Ala Ser Asp Gly Tyr Ile Phe Asn Pro Lys Asp Ile
 370 375 380

Val Glu Glu Thr Ala Thr Ala Tyr Ile Val Arg His Gly Asp His Phe
 385 390 395 400

His Tyr Ile Pro Lys Ser Asn Gln Ile Gly Gln Pro Thr Leu Pro Asn
 405 410 415

Asn Ser Leu Ala Thr Pro Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr
 420 425 430

Ser His Glu Lys His Glu Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg
 435 440 445

Ile Ile Ala Glu Asp Glu Ser Gly Phe Val Met Ser His Gly Asp His
 450 455 460

Asn His Tyr Phe Phe Lys Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala
 465 470 475 480

Ala Gln Lys His Leu Glu Glu Val Lys Thr Ser His Asn Gly Leu Asp
 485 490 495

Ser Leu Ser Ser His Glu Gln Asp Tyr Pro Gly Asn Ala Lys Glu Met
 500 505 510

Lys Asp Leu Asp Lys Lys Ile Glu Glu Lys Ile Ala Gly Ile Met Lys
 515 520 525

Gln Tyr Gly Val Lys Arg Glu Ser Ile Val Val Asn Lys Glu Lys Asn
 530 535 540

Ala Ile Ile Tyr Pro His Gly Asp His His His Ala Asp Pro Ile Asp
 545 550 555 560

Glu His Lys Pro Val Gly Ile Gly His Ser His Ser Asn Tyr Glu Leu
565 570 575

Phe Lys Pro Glu Glu Gly Val Ala Lys Lys Glu Gly Asn Lys Val Tyr
580 585 590

Thr Gly Glu Glu Leu Thr Asn Val Val Asn Leu Leu Lys Asn Ser Thr
595 600 605

Phe Asn Asn Gln Asn Phe Thr Leu Ala Asn Gly Gln Lys Arg Val Ser
610 615 620

Phe Ser Phe Pro Pro Glu Leu Glu Lys Lys Leu Gly Ile Asn Met Leu
625 630 635 640

Val Lys Leu Ile Thr Pro Asp Gly Lys Val Leu Glu Lys Val Ser Gly
645 650 655

Lys Val Phe Gly Glu Gly Val Gly Asn Ile Ala Asn Phe Glu Leu Asp
660 665 670

Gln Pro Tyr Leu Pro Gly Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys
675 680 685

Asp Tyr Pro Glu Val Ser Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser
690 695 700

Leu Ala Tyr Lys Met Ala Ser Gln Thr Ile Phe Tyr Pro Phe His Ala
705 710 715 720

Gly Asp Thr Tyr Leu Arg Val Asn Pro Gln Phe Ala Val Pro Lys Gly
725 730 735

Thr Asp Ala Leu Val Arg Val Phe Asp Glu Phe His Gly Asn Ala Tyr
740 745 750

Leu Glu Asn Asn Tyr Lys Val Gly Glu Ile Lys Leu Pro Ile Pro Lys
755 760 765

Leu Asn Gln Gly Thr Thr Arg Thr Ala Gly Asn Lys Ile Pro Val Thr
770 775 780

Phe Met Ala Asn Ala Tyr Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu
785 790 795 800

Val Pro Ile Leu Glu Lys Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu
805 810 815

Pro Gln Phe Lys Arg Asn Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu
820 825 830

Lys Val Glu Glu Pro Lys Thr Ser Glu Lys Val Glu Lys Glu Lys Leu
835 840 845

Ser Glu Thr Gly Asn Ser Thr Ser Asn Ser Thr Leu Glu Glu Val Pro
850 855 860

Thr Val Asp Pro Val Gln Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr
865 870 875 880

Gly Met Lys Leu Glu Asn Val Leu Phe Asn Met Asp Gly Thr Ile Glu
885 890 895

Leu Tyr Leu Pro Ser Gly Glu Val Ile Lys Lys Asn Met Ala Asp Phe
900 905 910

Thr Gly Glu Ala Pro Gln Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn
915 920 925

Gly Lys Val Ser Thr Gly Thr Val Glu Asn Gln Pro Thr Glu Asn Lys
930 935 940

Pro Ala Asp Ser Leu Pro Glu Ala Pro Asn Glu Lys Pro Val Lys Pro
945 950 955 960

Glu Asn Ser Thr Asp Asn Gly Met Leu Asn Pro Glu Gly Asn Val Gly
965 970 975

Ser Asp Pro Met Leu Asp Pro Ala Leu Glu Glu Ala Pro Ala Val Asp
980 985 990

Pro Val Gln Glu Lys Leu Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly
995 1000 1005

Leu Asp Ser Val Ile Phe Asn Met Asp Gly Thr Ile Glu Leu Arg
1010 1015 1020

Leu Pro Ser Gly Glu Val Ile Lys Lys Asn Leu Ser Asp Phe Ile
1025 1030 1035

Ala

<210> 7
<211> 840
<212> PRT
<213> Streptococcus pneumoniae

<400> 7

Met Lys Ile Asn Lys Lys Tyr Leu Ala Gly Ser Val Ala Thr Leu Val
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Leu Ser Val Cys Ala Tyr Glu Leu Gly Leu His Gln Ala Gln Thr Val
20 25 30

Lys Glu Asn Asn Arg Val Ser Tyr Ile Asp Gly Lys Gln Ala Thr Gln
35 40 45

Lys Thr Glu Asn Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly Ile
50 55 60

Asn Ala Glu Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr
65 70 75 80

Ser His Gly Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp
85 90 95

Ala Ile Ile Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu
100 105 110

Lys Asp Ser Asp Ile Val Asn Glu Ile Lys Gly Gly Tyr Val Ile Lys
115 120 125

Val Asn Gly Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp
130 135 140

Asn Val Arg Thr Lys Glu Glu Ile Asn Arg Gln Lys Gln Glu His Ser
145 150 155 160

Gln His Arg Glu Gly Gly Thr Ser Ala Asn Asp Gly Ala Val Ala Phe
165 170 175

Ala Arg Ser Gln Gly Arg Tyr Thr Thr Asp Asp Gly Tyr Ile Phe Asn
180 185 190

Ala Ser Asp Ile Ile Glu Asp Thr Gly Asp Ala Tyr Ile Val Pro His
195 200 205

Gly Asp His Tyr His Tyr Ile Pro Lys Asn Glu Leu Ser Ala Ser Glu
210 215 220

Leu Ala Ala Ala Glu Ala Phe Leu Ser Gly Arg Glu Asn Leu Ser Asn
225 230 235 240

Leu Arg Thr Tyr Arg Arg Gln Asn Ser Asp Asn Thr Pro Arg Thr Asn
245 250 255

Trp Val Pro Ser Val Ser Asn Pro Gly Thr Thr Asn Thr Asn Thr Ser
260 265 270

Asn Asn Ser Asn Thr Asn Ser Gln Ala Ser Gln Ser Asn Asp Ile Asp
275 280 285

Ser Leu Leu Lys Gln Leu Tyr Lys Leu Pro Leu Ser Gln Arg His Val
290 295 300

Glu Ser Asp Gly Leu Ile Phe Asp Pro Ala Gln Ile Thr Ser Arg Thr
305 310 315 320

Ala Arg Gly Val Ala Val Pro His Gly Asn His Tyr His Phe Ile Pro
325 330 335

Tyr Glu Gln Met Ser Glu Leu Glu Lys Arg Ile Ala Arg Ile Ile Pro
340 345 350

Leu Arg Tyr Arg Ser Asn His Trp Val Pro Asp Ser Arg Pro Glu Glu
355 360 365

Pro Ser Pro Gln Pro Thr Pro Glu Pro Ser Pro Ser Pro Gln Pro Ala
370 375 380

Pro Asn Pro Gln Pro Ala Pro Ser Asn Pro Ile Asp Glu Lys Leu Val
385 390 395 400

Lys Glu Ala Val Arg Lys Val Gly Asp Gly Tyr Val Phe Glu Glu Asn
405 410 415

Gly Val Ser Arg Tyr Ile Pro Ala Lys Asn Leu Ser Ala Glu Thr Ala
420 425 430

Ala Gly Ile Asp Ser Lys Leu Ala Lys Gln Glu Ser Leu Ser His Lys
435 440 445

Leu Gly Ala Lys Lys Thr Asp Leu Pro Ser Ser Asp Arg Glu Phe Tyr
450 455 460

Asn Lys Ala Tyr Asp Leu Leu Ala Arg Ile His Gln Asp Leu Leu Asp
465 470 475 480

Asn Lys Gly Arg Gln Val Asp Phe Glu Ala Leu Asp Asn Leu Leu Glu
485 490 495

Arg Leu Lys Asp Val Ser Ser Asp Lys Val Lys Leu Val Asp Asp Ile
500 505 510

Leu Ala Phe Leu Ala Pro Ile Arg His Pro Glu Arg Leu Gly Lys Pro
515 520 525

Asn Ala Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu
530 535 540

Ala Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Pro Arg Asp
545 550 555 560

Ile Thr Ser Asp Glu Gly Asp Ala Tyr Val Thr Pro His Met Thr His
565 570 575

Ser His Trp Ile Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala
580 585 590

Ala Gln Ala Tyr Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp
595 600 605

His Gln Asp Ser Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr
610 615 620

Asn Arg Val Lys Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr
625 630 635 640

Asn Leu Gln Tyr Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro
645 650 655

His Tyr Asp His Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly
660 665 670

Leu Tyr Glu Ala Pro Lys Gly Tyr Thr Leu Glu Asp Leu Leu Ala Thr
675 680 685

Val Lys Tyr Tyr Val Glu His Pro Asn Glu Arg Pro His Ser Asp Asn
690 695 700

Gly Phe Gly Asn Ala Ser Asp His Val Gln Arg Asn Lys Asn Gly Gln
705 710 715 720

Ala Asp Thr Asn Gln Thr Glu Lys Pro Ser Glu Glu Lys Pro Gln Thr
725 730 735

Glu Lys Pro Glu Glu Glu Thr Pro Arg Glu Glu Lys Pro Gln Ser Glu
740 745 750

Lys Pro Glu Ser Pro Lys Pro Thr Glu Glu Pro Glu Glu Glu Ser Pro
755 760 765

Glu Glu Ser Glu Glu Pro Gln Val Glu Thr Glu Lys Val Glu Glu Lys
770 775 780

Leu Arg Glu Ala Glu Asp Leu Leu Gly Lys Ile Gln Asp Pro Ile Ile
785 790 795 800

Lys Ser Asn Ala Lys Glu Thr Leu Thr Gly Leu Lys Asn Asn Leu Leu
805 810 815

Phe Gly Thr Gln Asp Asn Asn Thr Ile Met Ala Glu Ala Glu Lys Leu
820 825 830

Leu Ala Leu Leu Lys Glu Ser Lys

835

840

<210> 8
 <211> 838
 <212> PRT
 <213> Streptococcus pneumoniae

<400> 8

Met Lys Ile Asn Lys Lys Tyr Leu Ala Gly Ser Val Ala Val Leu Ala
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Leu Ser Val Cys Ser Tyr Glu Leu Gly Arg His Gln Ala Gly Gln Val
 20 25 30

Lys Lys Glu Ser Asn Arg Val Ser Tyr Ile Asp Gly Asp Gln Ala Gly
 35 40 45

Gln Lys Ala Glu Asn Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly
 50 55 60

Ile Asn Ala Glu Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val
 65 70 75 80

Thr Ser His Gly Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr
 85 90 95

Asp Ala Ile Ile Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln
 100 105 110

Leu Lys Asp Ser Asp Ile Val Asn Glu Ile Lys Gly Gly Tyr Val Ile
 115 120 125

Lys Val Asp Gly Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala
 130 135 140

Asp Asn Ile Arg Thr Lys Glu Glu Ile Lys Arg Gln Lys Gln Glu His
 145 150 155 160

Ser His Asn His Asn Ser Arg Ala Asp Asn Ala Val Ala Ala Ala Arg
 165 170 175

Ala Gln Gly Arg Tyr Thr Thr Asp Asp Gly Tyr Ile Phe Asn Ala Ser
 180 185 190

Asp Ile Ile Glu Asp Thr Gly Asp Ala Tyr Ile Val Pro His Gly Asp
195 200 205

His Tyr His Tyr Ile Pro Lys Asn Glu Leu Ser Ala Ser Glu Leu Ala
210 215 220

Ala Ala Glu Ala Tyr Trp Asn Gly Lys Gln Gly Ser Arg Pro Ser Ser
225 230 235 240

Ser Ser Ser Tyr Asn Ala Asn Pro Val Gln Pro Arg Leu Ser Glu Asn
245 250 255

His Asn Leu Thr Val Thr Pro Thr Tyr His Gln Asn Gln Gly Glu Asn
260 265 270

Ile Ser Ser Leu Leu Arg Glu Leu Tyr Ala Lys Pro Leu Ser Glu Arg
275 280 285

His Val Glu Ser Asp Gly Leu Ile Phe Asp Pro Ala Gln Ile Thr Ser
290 295 300

Arg Thr Ala Arg Gly Val Ala Val Pro His Gly Asn His Tyr His Phe
305 310 315 320

Ile Pro Tyr Glu Gln Met Ser Glu Leu Glu Lys Arg Ile Ala Arg Ile
325 330 335

Ile Pro Leu Arg Tyr Arg Ser Asn His Trp Val Pro Asp Ser Arg Pro
340 345 350

Glu Gln Pro Ser Pro Gln Ser Thr Pro Glu Pro Ser Pro Ser Leu Gln
355 360 365

Pro Ala Pro Asn Pro Gln Pro Ala Pro Ser Asn Pro Ile Asp Glu Lys
370 375 380

Leu Val Lys Glu Ala Val Arg Lys Val Gly Asp Gly Tyr Val Phe Glu
385 390 395 400

Glu Asn Gly Val Ser Arg Tyr Ile Pro Ala Lys Asp Leu Ser Ala Glu
405 410 415

Thr Ala Ala Gly Ile Asp Ser Lys Leu Ala Lys Gln Glu Ser Leu Ser
420 425 430

His Lys Leu Gly Ala Lys Lys Thr Asp Leu Pro Ser Ser Asp Arg Glu
435 440 445

Phe Tyr Asn Lys Ala Tyr Asp Leu Leu Ala Arg Ile His Gln Asp Leu
450 455 460

Leu Asp Asn Lys Gly Arg Gln Val Asp Phe Glu Val Leu Asp Asn Leu
465 470 475 480

Leu Glu Arg Leu Lys Asp Val Ser Ser Asp Lys Val Lys Leu Val Asp
485 490 495

Asp Ile Leu Ala Phe Leu Ala Pro Ile Arg His Pro Glu Arg Leu Gly
500 505 510

Lys Pro Asn Ala Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala
515 520 525

Lys Leu Ala Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Pro
530 535 540

Arg Asp Ile Thr Ser Asp Glu Gly Asp Ala Tyr Val Thr Pro His Met
545 550 555 560

Thr His Ser His Trp Ile Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg
565 570 575

Ala Ala Ala Gln Ala Tyr Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser
580 585 590

Thr Asp His Gln Asp Ser Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala
595 600 605

Ile Tyr Asn Arg Val Lys Ala Ala Lys Lys Val Pro Leu Asp Arg Met
610 615 620

Pro Tyr Asn Leu Gln Tyr Thr Val Glu Val Lys Asn Gly Ser Leu Ile
625 630 635 640

Ile Pro His Tyr Asp His Tyr His Asn Ile Lys Phe Glu Trp Phe Asp

645

650

655

Glu Gly Leu Tyr Glu Ala Pro Lys Gly Tyr Ser Leu Glu Asp Leu Leu
 660 665 670

Ala Thr Val Lys Tyr Tyr Val Glu His Pro Asn Glu Arg Pro His Ser
 675 680 685

Asp Asn Gly Phe Gly Asn Ala Ser Asp His Val Arg Lys Asn Lys Ala
 690 695 700

Asp Gln Asp Ser Lys Pro Asp Glu Asp Lys Glu His Asp Glu Val Ser
 705 710 715 720

Glu Pro Thr His Pro Glu Ser Asp Glu Lys Glu Asn His Ala Gly Leu
 725 730 735

Asn Pro Ser Ala Asp Asn Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu
 740 745 750

Thr Glu Glu Glu Ala Glu Asp Thr Thr Asp Glu Ala Glu Ile Pro Gln
 755 760 765

Val Glu Asn Ser Val Ile Asn Ala Lys Ile Ala Asp Ala Glu Ala Leu
 770 775 780

Leu Glu Lys Val Thr Asp Pro Ser Ile Arg Gln Asn Ala Met Glu Thr
 785 790 795 800

Leu Thr Gly Leu Lys Ser Ser Leu Leu Leu Gly Thr Lys Asp Asn Asn
 805 810 815

Thr Ile Ser Ala Glu Val Asp Ser Leu Leu Ala Leu Leu Lys Glu Ser
 820 825 830

Gln Pro Ala Pro Ile Gln
 835

<210> 9

<211> 2528

<212> DNA

<213> Streptococcus pneumoniae

<400> 9

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cagaaagaag gaattcaggc tgagcaaatt gtaatcaaaa ttacagatca gggctatgta	180
acgtcacacg gtgatcacta tcattactat aatgggaaag ttccttatga tgcctctctt	240
agtgaagaac tcttgatgaa ggatccaaac tatcaactta aagacgctga tattgtcaat	300
gaagtcaagg gtggttatat catcaaggtc gatggaaaat attatgtcta cctgaaagat	360
gcagctcatg ctgataatgt tcgaactaaa gatgaaatca atcgtcaaaa acaagaacat	420
gtcaaagata atgagaaggt taactctaata gttgctgtag caaggctctca gggacgatat	480
acgacaaatg atggttatgt ctttaatcca gctgatatta tcgaagatac gggtaatgct	540
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attaaggctg cgcaaaaaca tttagaggaa gttaaaaacta gtcataatgg attagattct	900
ttgtcatctc atgaacagga ttatccaagt aatgccaaag aaatgaaaga tttagataaa	960
aaaatcgaag aaaaaattgc tggcattatg aaacaatatg gtgtcaaacg tgaaagtatt	1020
gtcgtgaata aagaaaaaaa tgcgattatt tatccgcatg gagatcacca tcatgcagat	1080
ccgattgatg aacataaacc ggttggaatt ggtcattctc acagtaacta tgaactgttt	1140
aaacccgaag aaggagttgc taaaaaagaa gggaataaag tttatactgg agaagaatta	1200
acgaatgttg ttaatttggt aaaaaatagt acgtttaata atcaaaactt tactctagcc	1260
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aatatgctag taaaattaat aacaccagat ggaaaagtat tggagaaagt atctggtaaa	1380
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acatttacag ttccaacctc tttagcttac aaaatggcca gtcaaacgat tttctatcct	1560
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gatgctttag tcagagtgtt tgatgaattt catggaaatg cttattttaga aaataactat	1680
aaagttggtg aaatcaaatt accgattccg aaattaaacc aaggaacaac cagaacggcc	1740

ggaaataaaa ttctgtaac cttcatggca aatgcttatt tggacaatca atcgacttat 1800
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 caatttaaaa ggaataaagc acaagaaaac tcaaaacttg atgaaaaggt agaagaacca 1920
 aagactagtg agaaggtaga aaaagaaaaa ctttctgaaa ctgggaatag tactagtaat 1980
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 gaaagttatg ggatgaagct agaaaatgtc ttgtttaata tggacggaac aattgaatta 2100
 tatttaccat cgggagaagt cattaanaag aatatggcag attttacagg agaagcacct 2160
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 aaccaacca cagaaaataa accagcagat tctttaccag aggcacaaaa cgaaaaacct 2280
 gtaaaaccag aaaactcaac ggataatgga atgttgaatc cagaagggaa tgtggggagt 2340
 gaccctatgt tagattcagc attagaggaa gctccagcag tagatcctgt acaagaaaaa 2400
 ttagaaaaat ttacagctag ttacggatta ggcttagata gtgttatatt caatatggat 2460
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 tagcgtaa 2528

<210> 10
 <211> 840
 <212> PRT
 <213> Streptococcus pneumoniae

<400> 10

Cys Ala Tyr Ala Leu Asn Gln His Arg Ser Gln Glu Asn Lys Asp Asn
 1 5 10 15

Asn Arg Val Ser Tyr Val Asp Gly Ser Gln Ser Ser Gln Lys Ser Glu
 20 25 30

Asn Leu Thr Pro Asp Gln Val Ser Gln Lys Glu Gly Ile Gln Ala Glu
 35 40 45

Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val Thr Ser His Gly
 50 55 60

Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr Asp Ala Leu Phe
 65 70 75 80

Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln Leu Lys Asp Ala
85 90 95

Asp Ile Val Asn Glu Val Lys Gly Gly Tyr Ile Ile Lys Val Asp Gly
100 105 110

Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala Asp Asn Val Arg
115 120 125

Thr Lys Asp Glu Ile Asn Arg Gln Lys Gln Glu His Val Lys Asp Asn
130 135 140

Glu Lys Val Asn Ser Asn Val Ala Val Ala Arg Ser Gln Gly Arg Tyr
145 150 155 160

Thr Thr Asn Asp Gly Tyr Val Phe Asn Pro Ala Asp Ile Ile Glu Asp
165 170 175

Thr Gly Asn Ala Tyr Ile Val Pro His Gly Gly His Tyr His Tyr Ile
180 185 190

Pro Lys Ser Asp Leu Ser Ala Ser Glu Leu Ala Ala Lys Ala His
195 200 205

Leu Ala Gly Lys Asn Met Gln Pro Ser Gln Leu Ser Tyr Ser Ser Thr
210 215 220

Pro Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His
225 230 235 240

Glu Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp
245 250 255

Glu Ser Gly Phe Val Met Ser His Gly Asp His Asn His Tyr Phe Phe
260 265 270

Lys Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu
275 280 285

Glu Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser His
290 295 300

Glu Gln Asp Tyr Pro Ser Asn Ala Lys Glu Met Lys Asp Leu Asp Lys

305

310

315

320

Lys Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys
 325 330 335

Arg Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro
 340 345 350

His Gly Asp His His His Ala Asp Pro Ile Asp Glu His Lys Pro Val
 355 360 365

Gly Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu
 370 375 380

Gly Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu
 385 390 395 400

Thr Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn
 405 410 415

Phe Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro
 420 425 430

Glu Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr
 435 440 445

Pro Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu
 450 455 460

Gly Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro
 465 470 475 480

Gly Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val
 485 490 495

Ser Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met
 500 505 510

Ala Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu
 515 520 525

Arg Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val
 530 535 540

Arg Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr
 545 550 555 560

Lys Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr
 565 570 575

Thr Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala
 580 585 590

Tyr Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu Glu
 595 600 605

Lys Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg
 610 615 620

Asn Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys Val Glu Glu Pro
 625 630 635 640

Lys Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn
 645 650 655

Ser Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro Val
 660 665 670

Gln Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu
 675 680 685

Asn Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser
 690 695 700

Gly Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala Pro
 705 710 715 720

Gln Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser Thr
 725 730 735

Gly Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu
 740 745 750

Pro Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp
 755 760 765

Asn Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu
770 775 780

Asp Ser Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys
785 790 795 800

Leu Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile
805 810 815

Phe Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val
820 825 830

Ile Lys Lys Asn Leu Leu Ile Ser
835 840

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1 5 10 15

Gly Lys Val Pro Tyr Asp Ala Leu Phe Ser Glu Glu Leu Leu Met Lys
20 25 30

Asp Pro Asn Tyr Gln Leu Lys Asp Ala Asp Ile Val Asn Glu Val Lys
35 40 45

Gly Gly Tyr Ile Ile Lys Val Asp Gly Lys Tyr Tyr Val Tyr Leu Lys
50 55 60

Asp Ala Ala His Ala Asp Asn Val Arg Thr Lys Asp Glu Ile Asn Arg
65 70 75 80

Gln Lys Gln Glu His Val Lys Asp Asn Glu Lys Val Asn Ser
85 90

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<400> 12

Gly Ile Gln Ala Glu Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr
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Val Thr Ser His Gly Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro
20 25 30

Tyr Asp Ala Leu Phe Ser Glu Glu Leu Leu
35 40

<210> 13
<211> 39
<212> PRT
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<400> 13

Thr Ala Tyr Ile Val Arg His Gly Asp His Phe His Tyr Ile Pro Lys
1 5 10 15

Ser Asn Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr
20 25 30

Pro Ser Pro Ser Leu Pro Ile
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Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro Val Gln
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Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn

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25

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Val Leu Phe Asn
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Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val Ile Lys
1 5 10 15

Lys Asn Leu Ser Asp Phe Ile Ala
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<400> 16

Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe Asn Met Asp Gly Thr Ile
1 5 10 15

Glu Leu Arg Leu Pro Ser Gly Glu Val Ile Lys Lys Asn Leu Ser Asp
20 25 30

Phe Ile Ala
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Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu
1 5 10 15

Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe
20 25 30

Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val Ile
35 40 45

Lys Lys Asn Leu Ser Asp Phe Ile Ala
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<400> 18

Lys Val Glu Glu Pro Lys Thr Ser Glu Lys Val Glu Lys Glu Lys Leu
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Ser Glu Thr Gly Asn Ser Thr Ser Asn Ser Thr Leu Glu Glu Val Pro
20 25 30

Thr Val Asp Pro Val Gln Glu Lys
35 40

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<400> 19

Met Lys Asp Leu Asp Lys Lys Ile Glu Glu Lys Ile Ala Gly Ile Met
1 5 10 15

Lys Gln Tyr Gly Val Lys Arg Glu Ser Ile Val Val Asn Lys Glu Lys
20 25 30

Asn Ala Ile Ile Tyr Pro His Gly Asp His His His Ala Asp Pro Ile

35

40

45

Asp Glu His Lys Pro Val Gly Ile Gly His Ser His Ser Asn Tyr Glu
 50 55 60

Leu Phe Lys Pro Glu Glu Gly Val Ala Lys Lys Glu Gly Asn
 65 70 75

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<400> 20

Ala Ile Ile Tyr Pro His Gly Asp His His His Ala Asp Pro Ile Asp
 1 5 10 15

Glu His Lys Pro Val Gly Ile Gly His Ser His Ser Asn Tyr Glu Leu
 20 25 30

Phe Lys Pro Glu Glu Gly Val Ala Lys Lys Glu Gly Asn Lys Val Tyr
 35 40 45

Thr Gly Glu
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<400> 21

Ile Gln Val Ala Lys Leu Ala Gly Lys Tyr Thr Thr Glu Asp Gly Tyr
 1 5 10 15

Ile Phe Asp Pro Arg Asp Ile Thr Ser Asp Glu Gly Asp
 20 25

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<400> 22

Asp His Gln Asp Ser Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile
1 5 10 15

Tyr Asn Arg Val Lys Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro
20 25 30

Tyr Asn Leu Gln Tyr Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile
35 40 45

Pro His Tyr Asp His Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu
50 55 60

Gly Leu Tyr Glu Ala Pro Lys Gly Tyr Ser Leu Glu Asp Leu Leu Ala
65 70 75 80

Thr Val Lys Tyr Tyr Val
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<400> 23

Gly Leu Tyr Glu Ala Pro Lys Gly Tyr Ser Leu Glu Asp Leu Leu Ala
1 5 10 15

Thr Val Lys Tyr Tyr Val Glu His Pro Asn Glu Arg Pro His Ser Asp
20 25 30

Asn Gly Phe Gly Asn Ala Ser Asp His
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Leu Glu Lys Val Thr Asp Pro Ser Ile Arg Gln Asn Ala Met Glu Thr
20 25 30

Leu Thr Gly Leu Lys Ser Ser Leu Leu Leu Gly Thr Lys Asp Asn Asn
35 40 45

Thr Ile Ser Ala Glu Val Asp Ser Leu Leu Ala Leu Leu Lys Glu Ser
50 55 60

Gln Pro Ala Pro Ile
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<400> 25

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27

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gatctctaga ctactgctat tccttacgct atg

33

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<400> 27

atcactcgag cattacctgg ataatcctgt

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<400> 29

gatactcgag ctgctattcc ttac

24

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gaatctcgag ttaagctgct gctaattc

28

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gacgctcgag cgctatgaaa tcagataaat tc

32

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gacgctcgag ggcattacct ggataatcct gttcatg

37

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cagtagatct cttcatcatt tattgaaaag agg

33

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ttattttcttc catatggact tgacagaaga gcaaattaag

40

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<400> 35

cgccaagctt cgctatgaaa tcagataaat tc

32

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cgccaagctt ttccacaata taagtcgatt gatt

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ataagaatgc ggccgcttcc acaatataag tcgattgatt

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32

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<400> 42
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34

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cgccaagctt tagcgttacc aaaaccatta tc

32

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cgcctctaga ctactgtata ggagccgg

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catgccatgg atattcttgc cttcttagct cc

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gatgcatatg aatatgcaac cgagtcagtt aagc

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30

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<223> Unknown Organism

<400> 194
cggatctgca tgatggccat ctccatgcgg

30

<210> 195
<211> 43
<212> DNA
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<223> Unknown Organism

<400> 195

gtcatgagtc acggagactc caatcattat ttcttcaaga agg

43

<210> 196

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

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<400> 196

ccttcttgaa gaaataatga ttggagtctc cgtgactcat gac

43

<210> 197

<211> 45

<212> DNA

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<400> 197

atgagtcacg gagaccacaa ttcttatttc ttcaagaagg acttg

45

<210> 198

<211> 45

<212> DNA

<213> Artificial Sequence

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<223> Unknown Organism

<400> 198

caagtccttc ttgaagaaat aagaattgtg gtctccgtga ctcac

45

<210> 199

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 199

tacctcatta tgactcttac tctaacatca aatttgagtg gtttg

45

<210> 200

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 200

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45

<210> 201

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 201

taccttctta tgaccattac tctaacaatca aatttgagtg gtttg

45

<210> 202

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 202

aaaccactca aatttgatgt tagagtaatg gtcataagaa ggta

44

<210> 203

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 203

aacggtagtt taatcatacc ttctaaagac cattaccata acatc

45

<210> 204

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 204

gatgttatgg taatggtctt tagaaggat gattaaacta ccgtt

45

<210> 205
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
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<400> 205
cggtagttaa atcacacctc ataaggactc ttaccataac atcaaa

46

<210> 206
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<400> 206
tttgatgtta tggtaagagt ccttatgagg tatgattaaa ctaccg

46

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<400> 207
aacggtagtt taatcatacc tgaccattac cataacatca aatttg

46

<210> 208
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<220>
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<400> 208
caaatttgat gttatggtaa tggtcaggta tgattaaact accgtt

46

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<400> 209

aacggtagtt taatcatacc ttaccataac atcaaatttg agtgg

45

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<400> 210
ccactcaaat ttgatgttat ggtaaggat gattaaacta ccggt

45

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<400> 211
accgtagtt taatcatacc taacatcaaa ttgagtggg ttgac

45

<210> 212
<211> 45
<212> DNA
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<220>
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<400> 212
gtcaaaccac tcaaatttga tgtaggtat gattaaacta ccggt

45

<210> 213
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<212> DNA
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<220>
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<400> 213
cctatgtaac tccacatata acccatagcc actgg

35

<210> 214
<211> 35
<212> DNA
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<220>

<223> Unknown Organism

<400> 214

ccagtggcta tgggttatat gtggagttac atagg

35

<210> 215

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 215

cgtgaaagta ttgtcgtaaa taaagaaaaa aatgcg

36

<210> 216

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 216

cgcatttttt tctttattta cgacaatact ttcacg

36

<210> 217

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 217

catgaagaag atggttacgg ttctgatgct aaccgtatta tcgctgaag

49

<210> 218

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 218

cttcagcgat aatacgggta gcatcgaaac cgtaaccate ttcttctg

48

<210> 219

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 219

gaatcagggtt ttgtcatgag tgaccacaat cattatttct tc

42

<210> 220

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 220

gaagaaataa tgattgtggt cactcatgac aaaacctgat tc

42

<210> 221

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 221

gaagatgaat caggttttgt catgagtaat cattatttct tcaag

45

<210> 222

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

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<400> 222

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45

<210> 223

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 223

gaagatgaat caggttttgt catgagttat ttcttcaaga aggac

45

<210> 224
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<212> DNA
<213> Artificial Sequence

<220>
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<400> 224
gtccttcttg aagaaataac tcatgacaaa acctgattca tcttc

45

<210> 225
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<212> DNA
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<220>
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<400> 225
aaaatgcgat tatttatccg caccatcatg cagatccgat tg

42

<210> 226
<211> 42
<212> DNA
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<220>
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<400> 226
caatcggatc tgcgatgatgg tgcggataaa taatcgcatt tt

42

<210> 227
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Unknown Organism

<400> 227
aaaatgcgat tatttatccg gcagatccga ttgatgaaca taaac

45

<210> 228
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Unknown Organism

<400> 228

gtttatgttc atcaatcgga tctgccggat aaataatcgc atttt

45

<210> 229
<211> 45
<212> DNA
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<220>
<223> Unknown Organism

<400> 229
gatgctaacc gtataatcgc cgaagacgaa tcaggttttg tcatg

45

<210> 230
<211> 45
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<220>
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<400> 230
catgacaaaa cctgattcgt cttcggcgat tatacgggta gcatc

45

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<211> 43
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<220>
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<400> 231
cgccgaagac gaatccggct ttgtaatgag tcacggagac tcc

43

<210> 232
<211> 43
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<220>
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<400> 232
ggagtctccg tgactcatta caaagccgga ttcgtcttcg gcg

43

<210> 233
<211> 45
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<220>

<223> Unknown Organism

<400> 233

catctcatga acaggattat cccggcaacg ccaaagaaat gaaag

45

<210> 234

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

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<400> 234

ctttcatttc tttggcgttg ccgggataat cctgttcatg agatg

45

<210> 235

<211> 569

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 235

Met Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu
1 5 10 15

Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser His Glu
20 25 30

Gln Asp Tyr Pro Gly Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys
35 40 45

Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg
50 55 60

Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro His
65 70 75 80

Gly Asp His His His Ala Asp Pro Ile Asp Glu His Lys Pro Val Gly
85 90 95

Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly
100 105 110

Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr

115

120

125

Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe
 130 135 140

Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro Glu
 145 150 155 160

Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr Pro
 165 170 175

Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu Gly
 180 185 190

Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly
 195 200 205

Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser
 210 215 220

Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala
 225 230 235 240

Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg
 245 250 255

Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg
 260 265 270

Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys
 275 280 285

Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr
 290 295 300

Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala Tyr
 305 310 315 320

Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu Glu Lys
 325 330 335

Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn
 340 345 350

Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys Val Glu Glu Pro Lys
355 360 365

Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser
370 375 380

Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro Val Gln
385 390 395 400

Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn
405 410 415

Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly
420 425 430

Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala Pro Gln
435 440 445

Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser Thr Gly
450 455 460

Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro
465 470 475 480

Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn
485 490 495

Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp
500 505 510

Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu
515 520 525

Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe
530 535 540

Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val Ile
545 550 555 560

Lys Lys Asn Leu Ser Asp Phe Ile Ala
565

<210> 236
<211> 0
<212> PRT
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<220>
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<400> 236
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<223> Intentionally skipped sequence

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<223> Intentionally skipped sequence

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<222> (1)..(633)
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<220>
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<222> (1)..(633)
<223> Intentionally skipped sequence

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<220>
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<220>
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<222> (1)..(633)
<223> Intentionally skipped sequence

<400> 248
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<210> 249
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<220>
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<222> (1)..(633)
<223> Intentionally skipped sequence

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<210> 250
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<220>

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<400> 251

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<220>

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<222> (1)..(627)

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<400> 254
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<210> 255
<211> 569
<212> PRT
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<220>
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<400> 255

Met Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu
1 5 10 15

Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser His Glu
20 25 30

Gln Asp Tyr Pro Gly Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys
35 40 45

Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg
50 55 60

Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro His
65 70 75 80

Gly Asp His His His Ala Asp Pro Ile Asp Glu His Lys Pro Val Gly
85 90 95

Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly
100 105 110

Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr
115 120 125

Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe
130 135 140

Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro Glu
145 150 155 160

Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr Pro
165 170 175

Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu Gly
180 185 190

Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly
195 200 205

Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser
210 215 220

Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala
225 230 235 240

Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg
245 250 255

Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg
260 265 270

Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys
275 280 285

Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr
290 295 300

Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala Tyr
305 310 315 320

Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu Glu Lys
325 330 335

Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn
340 345 350

Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys Val Glu Glu Pro Lys
355 360 365

Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser
370 375 380

Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro Val Gln
385 390 395 400

Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn
405 410 415

Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly
420 425 430

Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala Pro Gln
435 440 445

Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser Thr Gly
450 455 460

Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro
465 470 475 480

Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn
485 490 495

Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp
500 505 510

Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu
515 520 525

Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe
530 535 540

Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val Ile
545 550 555 560

Lys Lys Asn Leu Ser Asp Phe Ile Ala

<210> 256
 <211> 569
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 256

Met Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu
 1 5 10 15

Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser His Glu
 20 25 30

Gln Asp Tyr Pro Gly Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys
 35 40 45

Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg
 50 55 60

Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro Ser
 65 70 75 80

Gly Asp Gly Thr Ser Ala Asp Pro Ile Asp Glu His Lys Pro Val Gly
 85 90 95

Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly
 100 105 110

Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr
 115 120 125

Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe
 130 135 140

Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro Glu
 145 150 155 160

Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr Pro
 165 170 175

Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu Gly
180 185 190

Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly
195 200 205

Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser
210 215 220

Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala
225 230 235 240

Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg
245 250 255

Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg
260 265 270

Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys
275 280 285

Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr
290 295 300

Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala Tyr
305 310 315 320

Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu Glu Lys
325 330 335

Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn
340 345 350

Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys Val Glu Glu Pro Lys
355 360 365

Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser
370 375 380

Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro Val Gln
385 390 395 400

Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn

405

410

415

Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly
 420 425 430

Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala Pro Gln
 435 440 445

Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser Thr Gly
 450 455 460

Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro
 465 470 475 480

Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn
 485 490 495

Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp
 500 505 510

Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu
 515 520 525

Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe
 530 535 540

Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val Ile
 545 550 555 560

Lys Lys Asn Leu Ser Asp Phe Ile Ala
 565

<210> 257

<211> 819

<212> DNA

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 257

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acagaagacg gttatatctt tgatactagt tggattaaaa aagatagttt gtctgaagct 120

gagagagcgg cagcccaggc ttatgctaaa gagaaaggtt tgaccctcc ttcgacagac 180

caccaggatt caggaaatac tgaggcaaaa ggagcagaag ctatctacaa ccgcgtgaaa 240
 gcagctaaga aggtgccact tgatcgtatg ccttacaatc ttcagtatac tgtagaagtc 300
 aaaaacggta gtttaatcat acctcattat gaccattacc ataacatcaa atttgagtgg 360
 tttgacgaag gcctttatga ggcacctaag gggatatagtc ttgaggatct tttggcgact 420
 gtcaagtact atgtcgaacc gcggaacgct agtgaccatg ttcgtaaaaa taaggcagac 480
 caagatagta aacctgatga agataaggaa catgatgaag taagtgagcc aactcacctt 540
 gaatctgatg aaaaagagaa tcacgctggt ttaaatecct cagcagataa tctttataaa 600
 ccaagcactg atacggaaga gacagaggaa gaagctgaag ataccacaga tgaggctgaa 660
 attcctggta cccttagtat tagacaaaat gctatggaga cattgactgg tctaaaaagt 720
 agtcttcttc tcggaacgaa agataataac actatttcag cagaagtaga tagtctcttg 780
 gctttgttaa aagaaagtca accggctcct atacagtag 819

<210> 258
 <211> 272
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Unknown Organism

<400> 258

Met Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
 1 5 10 15

Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Thr Ser Trp Ile
 20 25 30

Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr
 35 40 45

Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser
 50 55 60

Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys
 65 70 75 80

Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr
 85 90 95

Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro His Tyr Asp His
 100 105 110
 Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala
 115 120 125
 Pro Lys Gly Tyr Ser Leu Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr
 130 135 140
 Val Glu Pro Arg Asn Ala Ser Asp His Val Arg Lys Asn Lys Ala Asp
 145 150 155 160
 Gln Asp Ser Lys Pro Asp Glu Asp Lys Glu His Asp Glu Val Ser Glu
 165 170 175
 Pro Thr His Pro Glu Ser Asp Glu Lys Glu Asn His Ala Gly Leu Asn
 180 185 190
 Pro Ser Ala Asp Asn Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr
 195 200 205
 Glu Glu Glu Ala Glu Asp Thr Thr Asp Glu Ala Glu Ile Pro Gly Thr
 210 215 220
 Pro Ser Ile Arg Gln Asn Ala Met Glu Thr Leu Thr Gly Leu Lys Ser
 225 230 235 240
 Ser Leu Leu Leu Gly Thr Lys Asp Asn Asn Thr Ile Ser Ala Glu Val
 245 250 255
 Asp Ser Leu Leu Ala Leu Leu Lys Glu Ser Gln Pro Ala Pro Ile Gln
 260 265 270

<210> 259
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Unknown Organism

<400> 259
 ccgaattcca tatgcaaatt acctacactg atgatg

<210> 260
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Unknown Organism

<400> 260
ggactagtat caaagatata accgtcttc

29

<210> 261
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Unknown Organism

<400> 261
ggactagttg gattaataaaa gatagtttgt ctg

33

<210> 262
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Unknown Organism

<400> 262
ttcccgcggt tcgacatagt acttgacagt cg

32

<210> 263
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Unknown Organism

<400> 263
ttcccgcgga acgctagtga ccatgttcg

29

<210> 264
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Unknown Organism

<400> 264

cggggtacca ggaatttcag cctcatctgt g

31

<210> 265
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Unknown Organism

<400> 265
cccgggtaccc ctagtattag acaaaatgct atggag

36

<210> 266
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Unknown Organism

<400> 266
ggatcccggg aggtatgatt aaactaccg

29

<210> 267
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Unknown Organism

<400> 267
catgcccggg aacatcaaatttgagtgggtt tgac

34

<210> 268
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Unknown Organism

<400> 268
cttgatcgac atatgttggc aggcaagtac acaacag

37

<210> 269
<211> 45
<212> DNA
<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 269

aacggtagtt taatcatacc ttcttatgac cattaccata acatc

45

<210> 270

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 270

gatggttatgg taatgggtcat aagaagggtat gattaaacta ccggtt

45

<210> 271

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 271

aatcatacct tcttatgact cttaccataa catcaaattt gagtg

45

<210> 272

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 272

cactcaaatt tgatggttatg gtaagagtca taagaaggta tgatt

45

<210> 273

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 273

taccttctta tgactcttac tctaacatca aatttgagtg gtttg

45

<210> 274

<211> 45

<212> DNA

<213> Artificial Sequence
 <220>
 <223> Unknown Organism
 <400> 274
 caaaccactc aaatttgatg ttagagtaag agtcataaga aggta 45

<210> 275
 <211> 45
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Unknown Organism
 <400> 275
 aatcatacct cattatgact cttaccataa catcaaattt gagtg 45

<210> 276
 <211> 45
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Unknown Organism
 <400> 276
 cactcaaatt tgatgttatg gtaagagtca taatgaggta tgatt 45

<210> 277
 <211> 45
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Unknown Organism
 <400> 277
 tacctcatta tgaccattac tctaacaatca aatttgagtg gtttg 45

<210> 278
 <211> 45
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Unknown Organism
 <400> 278
 caaaccactc aaatttgatg ttagagtaat ggtcataatg aggta 45

<210> 279
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Unknown Organism

<400> 279
tacctcatta tgactcttac tctaacaatca aatttgagtg gtttg

45

<210> 280
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Unknown Organism

<400> 280
caaaccactc aaatttgatg ttagagtaag agtcataatg aggta

45

<210> 281
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Unknown Organism

<400> 281
tacctttctta tgaccattac tctaacaatca aatttgagtg gtttg

45

<210> 282
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Unknown Organism

<400> 282
aaaccactca aatttgatgt tagagtaatg gtcataagaa ggta

44

<210> 283
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Unknown Organism

<400> 283

aacggtagtt taatcatacc ttctaaagac cattaccata acatc

45

<210> 284

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 284

gatggttatgg taatggtctt tagaagggtat gattaaacta ccggtt

45

<210> 285

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 285

cggtagttta atcatacctc ataaggactc ttaccataac atcaaa

46

<210> 286

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 286

tttgatgtta tggtaagagt ccttatgagg tatgattaaa ctaccg

46

<210> 287

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 287

aacggtagtt taatcatacc tgaccattac cataacatca aatttg

46

<210> 288

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 288

caaatttgat gttatggtaa tggtcaggta tgattaaact accggt

46

<210> 289

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 289

aacggtagtt taatcatacc ttaccataac atcaaatttg agtgg

45

<210> 290

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 290

ccactcaaat ttgatgttat ggtaagggtat gattaaacta ccggt

45

<210> 291

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 291

accggtagtt taatcatacc taacatcaaa tttgagtggg ttgac

45

<210> 292

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 292

gtcaaaccac tcaaatttga tgttaggtat gattaaacta ccggt

45

<210> 293

<211> 272

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 293

Met Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
1 5 10 15

Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Thr Ser Trp Ile
20 25 30

Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr
35 40 45

Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser
50 55 60

Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys
65 70 75 80

Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr
85 90 95

Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro Ser Tyr Asp His
100 105 110

Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala
115 120 125

Pro Lys Gly Tyr Ser Leu Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr
130 135 140

Val Glu Pro Arg Asn Ala Ser Asp His Val Arg Lys Asn Lys Ala Asp
145 150 155 160

Gln Asp Ser Lys Pro Asp Glu Asp Lys Glu His Asp Glu Val Ser Glu
165 170 175

Pro Thr His Pro Glu Ser Asp Glu Lys Glu Asn His Ala Gly Leu Asn
180 185 190

Pro Ser Ala Asp Asn Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr
195 200 205

Glu Glu Glu Ala Glu Asp Thr Thr Asp Glu Ala Glu Ile Pro Gly Thr
210 215 220

Pro Ser Ile Arg Gln Asn Ala Met Glu Thr Leu Thr Gly Leu Lys Ser
225 230 235 240

Ser Leu Leu Leu Gly Thr Lys Asp Asn Asn Thr Ile Ser Ala Glu Val
245 250 255

Asp Ser Leu Leu Ala Leu Leu Lys Glu Ser Gln Pro Ala Pro Ile Gln
260 265 270

<210> 294

<211> 272

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 294

Met Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
1 5 10 15

Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Thr Ser Trp Ile
20 25 30

Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr
35 40 45

Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser
50 55 60

Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys
65 70 75 80

Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr
85 90 95

Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro His Tyr Asp Ser
100 105 110

Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala

115

120

125

Pro Lys Gly Tyr Ser Leu Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr
 130 135 140

Val Glu Pro Arg Asn Ala Ser Asp His Val Arg Lys Asn Lys Ala Asp
 145 150 155 160

Gln Asp Ser Lys Pro Asp Glu Asp Lys Glu His Asp Glu Val Ser Glu
 165 170 175

Pro Thr His Pro Glu Ser Asp Glu Lys Glu Asn His Ala Gly Leu Asn
 180 185 190

Pro Ser Ala Asp Asn Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr
 195 200 205

Glu Glu Glu Ala Glu Asp Thr Thr Asp Glu Ala Glu Ile Pro Gly Thr
 210 215 220

Pro Ser Ile Arg Gln Asn Ala Met Glu Thr Leu Thr Gly Leu Lys Ser
 225 230 235 240

Ser Leu Leu Leu Gly Thr Lys Asp Asn Asn Thr Ile Ser Ala Glu Val
 245 250 255

Asp Ser Leu Leu Ala Leu Leu Lys Glu Ser Gln Pro Ala Pro Ile Gln
 260 265 270

<210> 295

<211> 272

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 295

Met Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
 1 5 10 15

Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Thr Ser Trp Ile
 20 25 30

Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr
35 40 45

Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser
50 55 60

Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys
65 70 75 80

Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr
85 90 95

Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro His Tyr Asp His
100 105 110

Tyr Ser Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala
115 120 125

Pro Lys Gly Tyr Ser Leu Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr
130 135 140

Val Glu Pro Arg Asn Ala Ser Asp His Val Arg Lys Asn Lys Ala Asp
145 150 155 160

Gln Asp Ser Lys Pro Asp Glu Asp Lys Glu His Asp Glu Val Ser Glu
165 170 175

Pro Thr His Pro Glu Ser Asp Glu Lys Glu Asn His Ala Gly Leu Asn
180 185 190

Pro Ser Ala Asp Asn Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr
195 200 205

Glu Glu Glu Ala Glu Asp Thr Thr Asp Glu Ala Glu Ile Pro Gly Thr
210 215 220

Pro Ser Ile Arg Gln Asn Ala Met Glu Thr Leu Thr Gly Leu Lys Ser
225 230 235 240

Ser Leu Leu Leu Gly Thr Lys Asp Asn Asn Thr Ile Ser Ala Glu Val
245 250 255

Asp Ser Leu Leu Ala Leu Leu Lys Glu Ser Gln Pro Ala Pro Ile Gln

260

265

270

<210> 296
 <211> 272
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Unknown Organism

<400> 296

Met Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
 1 5 10 15

Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Thr Ser Trp Ile
 20 25 30

Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr
 35 40 45

Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser
 50 55 60

Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys
 65 70 75 80

Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr
 85 90 95

Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro Ser Tyr Asp Ser
 100 105 110

Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala
 115 120 125

Pro Lys Gly Tyr Ser Leu Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr
 130 135 140

Val Glu Pro Arg Asn Ala Ser Asp His Val Arg Lys Asn Lys Ala Asp
 145 150 155 160

Gln Asp Ser Lys Pro Asp Glu Asp Lys Glu His Asp Glu Val Ser Glu
 165 170 175

Pro Thr His Pro Glu Ser Asp Glu Lys Glu Asn His Ala Gly Leu Asn
180 185 190

Pro Ser Ala Asp Asn Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr
195 200 205

Glu Glu Glu Ala Glu Asp Thr Thr Asp Glu Ala Glu Ile Pro Gly Thr
210 215 220

Pro Ser Ile Arg Gln Asn Ala Met Glu Thr Leu Thr Gly Leu Lys Ser
225 230 235 240

Ser Leu Leu Leu Gly Thr Lys Asp Asn Asn Thr Ile Ser Ala Glu Val
245 250 255

Asp Ser Leu Leu Ala Leu Leu Lys Glu Ser Gln Pro Ala Pro Ile Gln
260 265 270

<210> 297

<211> 272

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 297

Met Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
1 5 10 15

Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Thr Ser Trp Ile
20 25 30

Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr
35 40 45

Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser
50 55 60

Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys
65 70 75 80

Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr
85 90 95

Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro Ser Tyr Asp Ser
100 105 110

Tyr Ser Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala
115 120 125

Pro Lys Gly Tyr Ser Leu Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr
130 135 140

Val Glu Pro Arg Asn Ala Ser Asp His Val Arg Lys Asn Lys Ala Asp
145 150 155 160

Gln Asp Ser Lys Pro Asp Glu Asp Lys Glu His Asp Glu Val Ser Glu
165 170 175

Pro Thr His Pro Glu Ser Asp Glu Lys Glu Asn His Ala Gly Leu Asn
180 185 190

Pro Ser Ala Asp Asn Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr
195 200 205

Glu Glu Glu Ala Glu Asp Thr Thr Asp Glu Ala Glu Ile Pro Gly Thr
210 215 220

Pro Ser Ile Arg Gln Asn Ala Met Glu Thr Leu Thr Gly Leu Lys Ser
225 230 235 240

Ser Leu Leu Leu Gly Thr Lys Asp Asn Asn Thr Ile Ser Ala Glu Val
245 250 255

Asp Ser Leu Leu Ala Leu Leu Lys Glu Ser Gln Pro Ala Pro Ile Gln
260 265 270

<210> 298

<211> 272

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 298

Met Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
1 5 10 15

Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Thr Ser Trp Ile
20 25 30

Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr
35 40 45

Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser
50 55 60

Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys
65 70 75 80

Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr
85 90 95

Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro His Tyr Asp Ser
100 105 110

Tyr Ser Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala
115 120 125

Pro Lys Gly Tyr Ser Leu Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr
130 135 140

Val Glu Pro Arg Asn Ala Ser Asp His Val Arg Lys Asn Lys Ala Asp
145 150 155 160

Gln Asp Ser Lys Pro Asp Glu Asp Lys Glu His Asp Glu Val Ser Glu
165 170 175

Pro Thr His Pro Glu Ser Asp Glu Lys Glu Asn His Ala Gly Leu Asn
180 185 190

Pro Ser Ala Asp Asn Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr
195 200 205

Glu Glu Glu Ala Glu Asp Thr Thr Asp Glu Ala Glu Ile Pro Gly Thr
210 215 220

Pro Ser Ile Arg Gln Asn Ala Met Glu Thr Leu Thr Gly Leu Lys Ser
225 230 235 240

Ser Leu Leu Leu Gly Thr Lys Asp Asn Asn Thr Ile Ser Ala Glu Val
245 250 255

Asp Ser Leu Leu Ala Leu Leu Lys Glu Ser Gln Pro Ala Pro Ile Gln
260 265 270

<210> 299

<211> 272

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 299

Met Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
1 5 10 15

Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Thr Ser Trp Ile
20 25 30

Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr
35 40 45

Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser
50 55 60

Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys
65 70 75 80

Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr
85 90 95

Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro Ser Tyr Asp His
100 105 110

Tyr Ser Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala
115 120 125

Pro Lys Gly Tyr Ser Leu Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr
130 135 140

Val Glu Pro Arg Asn Ala Ser Asp His Val Arg Lys Asn Lys Ala Asp
145 150 155 160

Gln Asp Ser Lys Pro Asp Glu Asp Lys Glu His Asp Glu Val Ser Glu
165 170 175

Pro Thr His Pro Glu Ser Asp Glu Lys Glu Asn His Ala Gly Leu Asn
180 185 190

Pro Ser Ala Asp Asn Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr
195 200 205

Glu Glu Glu Ala Glu Asp Thr Thr Asp Glu Ala Glu Ile Pro Gly Thr
210 215 220

Pro Ser Ile Arg Gln Asn Ala Met Glu Thr Leu Thr Gly Leu Lys Ser
225 230 235 240

Ser Leu Leu Leu Gly Thr Lys Asp Asn Asn Thr Ile Ser Ala Glu Val
245 250 255

Asp Ser Leu Leu Ala Leu Leu Lys Glu Ser Gln Pro Ala Pro Ile Gln
260 265 270

<210> 300

<211> 272

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 300

Met Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
1 5 10 15

Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Thr Ser Trp Ile
20 25 30

Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr
35 40 45

Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser
50 55 60

Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys

65

70

75

80

Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr
 85 90 95

Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro Ser Lys Asp His
 100 105 110

Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala
 115 120 125

Pro Lys Gly Tyr Ser Leu Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr
 130 135 140

Val Glu Pro Arg Asn Ala Ser Asp His Val Arg Lys Asn Lys Ala Asp
 145 150 155 160

Gln Asp Ser Lys Pro Asp Glu Asp Lys Glu His Asp Glu Val Ser Glu
 165 170 175

Pro Thr His Pro Glu Ser Asp Glu Lys Glu Asn His Ala Gly Leu Asn
 180 185 190

Pro Ser Ala Asp Asn Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr
 195 200 205

Glu Glu Glu Ala Glu Asp Thr Thr Asp Glu Ala Glu Ile Pro Gly Thr
 210 215 220

Pro Ser Ile Arg Gln Asn Ala Met Glu Thr Leu Thr Gly Leu Lys Ser
 225 230 235 240

Ser Leu Leu Leu Gly Thr Lys Asp Asn Asn Thr Ile Ser Ala Glu Val
 245 250 255

Asp Ser Leu Leu Ala Leu Leu Lys Glu Ser Gln Pro Ala Pro Ile Gln
 260 265 270

<210> 301

<211> 272

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 301

Met Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
1 5 10 15

Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Thr Ser Trp Ile
20 25 30

Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr
35 40 45

Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser
50 55 60

Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys
65 70 75 80

Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr
85 90 95

Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro His Lys Asp Ser
100 105 110

Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala
115 120 125

Pro Lys Gly Tyr Ser Leu Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr
130 135 140

Val Glu Pro Arg Asn Ala Ser Asp His Val Arg Lys Asn Lys Ala Asp
145 150 155 160

Gln Asp Ser Lys Pro Asp Glu Asp Lys Glu His Asp Glu Val Ser Glu
165 170 175

Pro Thr His Pro Glu Ser Asp Glu Lys Glu Asn His Ala Gly Leu Asn
180 185 190

Pro Ser Ala Asp Asn Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr
195 200 205

Glu Glu Glu Ala Glu Asp Thr Thr Asp Glu Ala Glu Ile Pro Gly Thr

210

215

220

Pro Ser Ile Arg Gln Asn Ala Met Glu Thr Leu Thr Gly Leu Lys Ser
 225 230 235 240

Ser Leu Leu Leu Gly Thr Lys Asp Asn Asn Thr Ile Ser Ala Glu Val
 245 250 255

Asp Ser Leu Leu Ala Leu Leu Lys Glu Ser Gln Pro Ala Pro Ile Gln
 260 265 270

<210> 302

<211> 270

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 302

Met Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
 1 5 10 15

Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Thr Ser Trp Ile
 20 25 30

Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr
 35 40 45

Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser
 50 55 60

Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys
 65 70 75 80

Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr
 85 90 95

Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro Asp His Tyr His
 100 105 110

Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala Pro Lys
 115 120 125

Gly Tyr Ser Leu Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr Val Glu
130 135 140

Pro Arg Asn Ala Ser Asp His Val Arg Lys Asn Lys Ala Asp Gln Asp
145 150 155 160

Ser Lys Pro Asp Glu Asp Lys Glu His Asp Glu Val Ser Glu Pro Thr
165 170 175

His Pro Glu Ser Asp Glu Lys Glu Asn His Ala Gly Leu Asn Pro Ser
180 185 190

Ala Asp Asn Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr Glu Glu
195 200 205

Glu Ala Glu Asp Thr Thr Asp Glu Ala Glu Ile Pro Gly Thr Pro Ser
210 215 220

Ile Arg Gln Asn Ala Met Glu Thr Leu Thr Gly Leu Lys Ser Ser Leu
225 230 235 240

Leu Leu Gly Thr Lys Asp Asn Asn Thr Ile Ser Ala Glu Val Asp Ser
245 250 255

Leu Leu Ala Leu Leu Lys Glu Ser Gln Pro Ala Pro Ile Gln
260 265 270

<210> 303

<211> 268

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 303

Met Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
1 5 10 15

Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Thr Ser Trp Ile
20 25 30

Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr
35 40 45

Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser
 50 55 60

Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys
 65 70 75 80

Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr
 85 90 95

Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro Tyr His Asn Ile
 100 105 110

Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala Pro Lys Gly Tyr
 115 120 125

Ser Leu Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr Val Glu Pro Arg
 130 135 140

Asn Ala Ser Asp His Val Arg Lys Asn Lys Ala Asp Gln Asp Ser Lys
 145 150 155 160

Pro Asp Glu Asp Lys Glu His Asp Glu Val Ser Glu Pro Thr His Pro
 165 170 175

Glu Ser Asp Glu Lys Glu Asn His Ala Gly Leu Asn Pro Ser Ala Asp
 180 185 190

Asn Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr Glu Glu Glu Ala
 195 200 205

Glu Asp Thr Thr Asp Glu Ala Glu Ile Pro Gly Thr Pro Ser Ile Arg
 210 215 220

Gln Asn Ala Met Glu Thr Leu Thr Gly Leu Lys Ser Ser Leu Leu Leu
 225 230 235 240

Gly Thr Lys Asp Asn Asn Thr Ile Ser Ala Glu Val Asp Ser Leu Leu
 245 250 255

Ala Leu Leu Lys Glu Ser Gln Pro Ala Pro Ile Gln
 260 265

<210> 304
<211> 266
<212> PRT
<213> Artificial Sequence

<220>
<223> Unknown Organism

<400> 304

Met Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
1 5 10 15

Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Thr Ser Trp Ile
20 25 30

Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr
35 40 45

Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser
50 55 60

Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys
65 70 75 80

Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr
85 90 95

Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro Asn Ile Lys Phe
100 105 110

Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala Pro Lys Gly Tyr Ser Leu
115 120 125

Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr Val Glu Pro Arg Asn Ala
130 135 140

Ser Asp His Val Arg Lys Asn Lys Ala Asp Gln Asp Ser Lys Pro Asp
145 150 155 160

Glu Asp Lys Glu His Asp Glu Val Ser Glu Pro Thr His Pro Glu Ser
165 170 175

Asp Glu Lys Glu Asn His Ala Gly Leu Asn Pro Ser Ala Asp Asn Leu
180 185 190

Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr Glu Glu Glu Ala Glu Asp
195 200 205

Thr Thr Asp Glu Ala Glu Ile Pro Gly Thr Pro Ser Ile Arg Gln Asn
210 215 220

Ala Met Glu Thr Leu Thr Gly Leu Lys Ser Ser Leu Leu Leu Gly Thr
225 230 235 240

Lys Asp Asn Asn Thr Ile Ser Ala Glu Val Asp Ser Leu Leu Ala Leu
245 250 255

Leu Lys Glu Ser Gln Pro Ala Pro Ile Gln
260 265

<210> 305
<211> 0
<212> PRT
<213> Artificial Sequence

<220>
<223> Unknown Organism

<220>
<221> MISC_FEATURE
<222> (1)..(906)
<223> Intentionally skipped sequence

<400> 305
000
<210> 306
<211> 0
<212> PRT
<213> Artificial Sequence

<220>
<223> Unknown Organism

<220>
<221> MISC_FEATURE
<222> (1)..(906)
<223> Intentionally skipped sequence

<400> 306
000
<210> 307
<211> 0
<212> PRT
<213> Artificial Sequence

<220>
<223> Unknown Organism

<220>
<221> MISC_FEATURE
<222> (1)..(906)
<223> Intentionally skipped sequence

<400> 307
000
<210> 308
<211> 0
<212> PRT
<213> Artificial Sequence

<220>
<223> Unknown Organism

<220>
<221> MISC_FEATURE
<222> (1)..(906)
<223> Intentionally skipped sequence

<400> 308
000
<210> 309
<211> 0
<212> PRT
<213> Artificial Sequence

<220>
<223> Unknown Organism

<220>
<221> MISC_FEATURE
<222> (1)..(906)
<223> Intentionally skipped sequence

<400> 309
000
<210> 310
<211> 0
<212> PRT
<213> Artificial Sequence

<220>
<223> Unknown Organism

<220>
<221> MISC_FEATURE
<222> (1)..(906)
<223> Intentionally skipped sequence

<400> 310
000
<210> 311
<211> 0
<212> PRT
<213> Artificial Sequence

<220>
<223> Unknown Organism

<220>
<221> MISC_FEATURE
<222> (1)..(900)
<223> Intentionally skipped sequence

<400> 311
000
<210> 312
<211> 0
<212> PRT
<213> Artificial Sequence

<220>
<223> Unknown Organism

<220>
<221> MISC_FEATURE
<222> (1)..(900)
<223> Intentionally skipped sequence

<400> 312
000
<210> 313
<211> 0
<212> PRT
<213> Artificial Sequence

<220>
<223> Unknown Sequence

<220>
<221> MISC_FEATURE
<222> (1)..(900)
<223> Intentionally skipped sequence

<400> 313
000
<210> 314
<211> 0
<212> PRT
<213> Artificial Sequence

<220>

<223> Unknown Organism
 <220>
 <221> MISC_FEATURE
 <222> (1)..(894)
 <223> Intentionally skipped sequence

 <400> 314
 000
 <210> 315
 <211> 0
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Unknown Organism

 <220>
 <221> MISC_FEATURE
 <222> (1)..(894)
 <223> Intentionally skipped sequence

 <400> 315
 000
 <210> 316
 <211> 0
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Unknown Organism

 <220>
 <221> MISC_FEATURE
 <222> (1)..(888)
 <223> Intentionally skipped sequence

 <400> 316
 000
 <210> 317
 <211> 0
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Unknown Organism

 <220>
 <221> MISC_FEATURE
 <222> (1)..(900)
 <223> Intentionally skipped sequence

 <400> 317

000
<210> 318
<211> 0
<212> PRT
<213> Artificial Sequence

<220>
<223> Unknown Organism

<220>
<221> MISC_FEATURE
<222> (1)..(894)
<223> Intentionally skipped sequence

<400> 318
000
<210> 319
<211> 0
<212> PRT
<213> Artificial Sequence

<220>
<223> Unknown Organism

<220>
<221> MISC_FEATURE
<222> (1)..(900)
<223> Intentionally skipped sequence

<400> 319
000
<210> 320
<211> 0
<212> PRT
<213> Artificial Sequence

<220>
<223> Unknown Organism

<220>
<221> MISC_FEATURE
<222> (1)..(894)
<223> Intentionally skipped sequence

<400> 320
000
<210> 321
<211> 0
<212> PRT
<213> Artificial Sequence

<220>
<223> Unknown Organism

<220>
<221> MISC_FEATURE
<222> (1)..(901)
<223> Intentionally skipped sequence

<400> 321
000
<210> 322
<211> 0
<212> PRT
<213> Artificial Sequence

<220>
<223> Unknown Sequence

<220>
<221> MISC_FEATURE
<222> (1)..(895)
<223> Intentionally skipped sequence

<400> 322
000
<210> 323
<211> 0
<212> PRT
<213> Artificial Sequence

<220>
<223> Unknown Organism

<220>
<221> MISC_FEATURE
<222> (1)..(901)
<223> Intentionally skipped sequence

<400> 323
000
<210> 324
<211> 0
<212> PRT
<213> Artificial Sequence

<220>
<223> Unknown Organism

<220>
<221> MISC_FEATURE
<222> (1)..(895)
<223> Intentionally skipped sequence

<400> 324
000
<210> 325

<211> 0
<212> PRT
<213> Artificial Sequence

<220>
<223> Unknown Organism

<220>
<221> MISC_FEATURE
<222> (1)..(895)
<223> Intentionally skipped sequence

<400> 325
000
<210> 326
<211> 0
<212> PRT
<213> Artificial Sequence

<220>
<223> Unknown Organism

<220>
<221> MISC_FEATURE
<222> (1)..(889)
<223> Intentionally skipped sequence

<400> 326
000
<210> 327
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Unknown Organism

<400> 327
atatgggccc caaattacct acactgatga tgagattcag g

41

<210> 328
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Unknown Organism

<400> 328
ataagaatgc ggccgcctac tgtataggag ccggttgact ttc

43

<210> 329
<211> 33

<212> DNA
<213> Artificial Sequence

<220>
<223> Unknown Organism

<400> 329
ccgaattcca tatgcaaatt gggcaaccga etc

33

<210> 330
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Unknown Organism

<400> 330
atatggggccc caaattgggc aaccgactc

29

<210> 331
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Unknown Organism

<400> 331
ataagaatgc ggccgcttac gctatgaaat cagataaatt c

41

<210> 332
<211> 906
<212> PRT
<213> Artificial Sequence

<220>
<223> Unknown Organism

<400> 332

Met Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
1 5 10 15

Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Thr Ser Trp Ile
20 25 30

Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr
35 40 45

Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser

50

55

60

Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys
65 70 75 80

Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr
85 90 95

Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro Ser Tyr Asp His
100 105 110

Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala
115 120 125

Pro Lys Gly Tyr Ser Leu Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr
130 135 140

Val Glu Pro Arg Asn Ala Ser Asp His Val Arg Lys Asn Lys Ala Asp
145 150 155 160

Gln Asp Ser Lys Pro Asp Glu Asp Lys Glu His Asp Glu Val Ser Glu
165 170 175

Pro Thr His Pro Glu Ser Asp Glu Lys Glu Asn His Ala Gly Leu Asn
180 185 190

Pro Ser Ala Asp Asn Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr
195 200 205

Glu Glu Glu Ala Glu Asp Thr Thr Asp Glu Ala Glu Ile Pro Gly Thr
210 215 220

Pro Ser Ile Arg Gln Asn Ala Met Glu Thr Leu Thr Gly Leu Lys Ser
225 230 235 240

Ser Leu Leu Leu Gly Thr Lys Asp Asn Asn Thr Ile Ser Ala Glu Val
245 250 255

Asp Ser Leu Leu Ala Leu Leu Lys Glu Ser Gln Pro Ala Pro Ile Gln
260 265 270

Gly Pro Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr
275 280 285

Pro Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His
290 295 300

Glu Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp
305 310 315 320

Glu Ser Gly Phe Val Met Ser His Gly Asp Ser Asn His Tyr Phe Phe
325 330 335

Lys Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu
340 345 350

Glu Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser His
355 360 365

Glu Gln Asp Tyr Pro Gly Asn Ala Lys Glu Met Lys Asp Leu Asp Lys
370 375 380

Lys Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys
385 390 395 400

Arg Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro
405 410 415

Ser Gly Asp His His His Ala Asp Pro Ile Asp Glu His Lys Pro Val
420 425 430

Gly Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu
435 440 445

Gly Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu
450 455 460

Thr Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn
465 470 475 480

Phe Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro
485 490 495

Glu Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr
500 505 510

Pro Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu
515 520 525

Gly Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro
530 535 540

Gly Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val
545 550 555 560

Ser Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met
565 570 575

Ala Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu
580 585 590

Arg Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val
595 600 605

Arg Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr
610 615 620

Lys Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr
625 630 635 640

Thr Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala
645 650 655

Tyr Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu Glu
660 665 670

Lys Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg
675 680 685

Asn Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys Val Glu Glu Pro
690 695 700

Lys Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn
705 710 715 720

Ser Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro Val
725 730 735

Gln Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu
740 745 750

Asn Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser
755 760 765

Gly Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala Pro
770 775 780

Gln Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser Thr
785 790 795 800

Gly Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu
805 810 815

Pro Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp
820 825 830

Asn Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu
835 840 845

Asp Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys
850 855 860

Leu Glu Lys Phe Thr Ala Ser-Tyr Gly Leu Gly Leu Asp Ser Val Ile
865 870 875 880

Phe Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val
885 890 895

Ile Lys Lys Asn Leu Ser Asp Phe Ile Ala
900 905

<210> 333

<211> 900

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 333

Met Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr Pro
1 5 10 15

Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His Glu
 20 25 30

Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp Glu
 35 40 45

Ser Gly Phe Val Met Ser His Gly Asp Ser Asn His Tyr Phe Phe Lys
 50 55 60

Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu
 65 70 75 80

Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser His Glu
 85 90 95

Gln Asp Tyr Pro Gly Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys
 100 105 110

Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg
 115 120 125

Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro Ser
 130 135 140

Gly Asp His His His Ala Asp Pro Ile Asp Glu His Lys Pro Val Gly
 145 150 155 160

Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly
 165 170 175

Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr
 180 185 190

Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe
 195 200 205

Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro Glu
 210 215 220

Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr Pro
 225 230 235 240

Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu Gly
245 250 255

Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly
260 265 270

Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser
275 280 285

Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala
290 295 300

Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg
305 310 315 320

Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg
325 330 335

Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys
340 345 350

Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr
355 360 365

Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala Tyr
370 375 380

Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu Glu Lys
385 390 395 400

Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn
405 410 415

Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys Val Glu Glu Pro Lys
420 425 430

Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser
435 440 445

Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro Val Gln
450 455 460

Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn

465

470

475

480

Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly
 485 490 495

Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala Pro Gln
 500 505 510

Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser Thr Gly
 515 520 525

Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro
 530 535 540

Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn
 545 550 555 560

Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp
 565 570 575

Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu
 580 585 590

Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe
 595 600 605

Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val Ile
 610 615 620

Lys Lys Asn Leu Ser Asp Phe Ile Ala Gly Pro Gln Ile Thr Tyr Thr
 625 630 635 640

Asp Asp Glu Ile Gln Val Ala Lys Leu Ala Gly Lys Tyr Thr Thr Glu
 645 650 655

Asp Gly Tyr Ile Phe Asp Thr Ser Trp Ile Lys Lys Asp Ser Leu Ser
 660 665 670

Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr Ala Lys Glu Lys Gly Leu
 675 680 685

Thr Pro Pro Ser Thr Asp His Gln Asp Ser Gly Asn Thr Glu Ala Lys
 690 695 700

Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys Ala Ala Lys Lys Val Pro
705 710 715 720

Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr Thr Val Glu Val Lys Asn
725 730 735

Gly Ser Leu Ile Ile Pro Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly
740 745 750

Leu Tyr Glu Ala Pro Lys Gly Tyr Ser Leu Glu Asp Leu Leu Ala Thr
755 760 765

Val Lys Tyr Tyr Val Glu Pro Arg Asn Ala Ser Asp His Val Arg Lys
770 775 780

Asn Lys Ala Asp Gln Asp Ser Lys Pro Asp Glu Asp Lys Glu His Asp
785 790 795 800

Glu Val Ser Glu Pro Thr His Pro Glu Ser Asp Glu Lys Glu Asn His
805 810 815

Ala Gly Leu Asn Pro Ser Ala Asp Asn Leu Tyr Lys Pro Ser Thr Asp
820 825 830

Thr Glu Glu Thr Glu Glu Glu Ala Glu Asp Thr Thr Asp Glu Ala Glu
835 840 845

Ile Pro Gly Thr Pro Ser Ile Arg Gln Asn Ala Met Glu Thr Leu Thr
850 855 860

Gly Leu Lys Ser Ser Leu Leu Leu Gly Thr Lys Asp Asn Asn Thr Ile
865 870 875 880

Ser Ala Glu Val Asp Ser Leu Leu Ala Leu Leu Lys Glu Ser Gln Pro
885 890 895

Ala Pro Ile Gln
900

<210> 334

<211> 900

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 334

Met Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
1 5 10 15

Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Thr Ser Trp Ile
20 25 30

Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr
35 40 45

Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser
50 55 60

Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys
65 70 75 80

Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr
85 90 95

Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro Asn Ile Lys Phe
100 105 110

Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala Pro Lys Gly Tyr Ser Leu
115 120 125

Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr Val Glu Pro Arg Asn Ala
130 135 140

Ser Asp His Val Arg Lys Asn Lys Ala Asp Gln Asp Ser Lys Pro Asp
145 150 155 160

Glu Asp Lys Glu His Asp Glu Val Ser Glu Pro Thr His Pro Glu Ser
165 170 175

Asp Glu Lys Glu Asn His Ala Gly Leu Asn Pro Ser Ala Asp Asn Leu
180 185 190

Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr Glu Glu Glu Ala Glu Asp
195 200 205

Thr Thr Asp Glu Ala Glu Ile Pro Gly Thr Pro Ser Ile Arg Gln Asn
210 215 220

Ala Met Glu Thr Leu Thr Gly Leu Lys Ser Ser Leu Leu Leu Gly Thr
225 230 235 240

Lys Asp Asn Asn Thr Ile Ser Ala Glu Val Asp Ser Leu Leu Ala Leu
245 250 255

Leu Lys Glu Ser Gln Pro Ala Pro Ile Gln Gly Pro Gln Ile Gly Gln
260 265 270

Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr Pro Ser Pro Ser Leu Pro
275 280 285

Ile Asn Pro Gly Thr Ser His Glu Lys His Glu Glu Asp Gly Tyr Gly
290 295 300

Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp Glu Ser Gly Phe Val Met
305 310 315 320

Ser His Gly Asp Ser Asn His Tyr Phe Phe Lys Lys Asp Leu Thr Glu
325 330 335

Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu Glu Val Lys Thr Ser
340 345 350

His Asn Gly Leu Asp Ser Leu Ser Ser His Glu Gln Asp Tyr Pro Gly
355 360 365

Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys Ile Glu Glu Lys Ile
370 375 380

Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg Glu Ser Ile Val Val
385 390 395 400

Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro Ser Gly Asp His His His
405 410 415

Ala Asp Pro Ile Asp Glu His Lys Pro Val Gly Ile Gly His Ser His
420 425 430

Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly Val Ala Lys Lys Glu
435 440 445

Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr Asn Val Val Asn Leu
450 455 460

Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe Thr Leu Ala Asn Gly
465 470 475 480

Gln Lys Arg Val Ser Phe Ser Phe Pro Pro Glu Leu Glu Lys Lys Leu
485 490 495

Gly Ile Asn Met Leu Val Lys Leu Ile Thr Pro Asp Gly Lys Val Leu
500 505 510

Glu Lys Val Ser Gly Lys Val Phe Gly Glu Gly Val Gly Asn Ile Ala
515 520 525

Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly Gln Thr Phe Lys Tyr
530 535 540

Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser Tyr Asp Gly Thr Phe
545 550 555 560

Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala Ser Gln Thr Ile Phe
565 570 575

Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg Val Asn Pro Gln Phe
580 585 590

Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg Val Phe Asp Glu Phe
595 600 605

His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys Val Gly Glu Ile Lys
610 615 620

Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr Arg Thr Ala Gly Asn
625 630 635 640

Lys Ile Pro Val Thr Phe Met Ala Asn Ala Tyr Leu Asp Asn Gln Ser
645 650 655

Thr Tyr Ile Val Glu Val Pro Ile Leu Glu Lys Glu Asn Gln Thr Asp
660 665 670

Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn Lys Ala Gln Glu Asn
675 680 685

Ser Lys Leu Asp Glu Lys Val Glu Glu Pro Lys Thr Ser Glu Lys Val
690 695 700

Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser Thr Ser Asn Ser Thr
705 710 715 720

Leu Glu Glu Val Pro Thr Val Asp Pro Val Gln Glu Lys Val Ala Lys
725 730 735

Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn Val Leu Phe Asn Met
740 745 750

Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly Glu Val Ile Lys Lys
755 760 765

Asn Met Ala Asp Phe Thr Gly Glu Ala Pro Gln Gly Asn Gly Glu Asn
770 775 780

Lys Pro Ser Glu Asn Gly Lys Val Ser Thr Gly Thr Val Glu Asn Gln
785 790 795 800

Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro Glu Ala Pro Asn Glu
805 810 815

Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn Gly Met Leu Asn Pro
820 825 830

Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp Pro Ala Leu Glu Glu
835 840 845

Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu Glu Lys Phe Thr Ala
850 855 860

Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe Asn Met Asp Gly Thr
865 870 875 880

Ile Glu Leu Arg Leu Pro Ser Gly Glu Val Ile Lys Lys Asn Leu Ser

885

890

895

Asp Phe Ile Ala
900

<210> 335
<211> 900
<212> PRT
<213> Artificial Sequence

<220>
<223> Unknown Organism

<400> 335

Met Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
1 5 10 15

Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Thr Ser Trp Ile
20 25 30

Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr
35 40 45

Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser
50 55 60

Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys
65 70 75 80

Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr
85 90 95

Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro Ser Tyr Asp His
100 105 110

Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala
115 120 125

Pro Lys Gly Tyr Ser Leu Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr
130 135 140

Val Glu Pro Arg Asn Ala Ser Asp His Val Arg Lys Asn Lys Ala Asp
145 150 155 160

Gln Asp Ser Lys Pro Asp Glu Asp Lys Glu His Asp Glu Val Ser Glu
165 170 175

Pro Thr His Pro Glu Ser Asp Glu Lys Glu Asn His Ala Gly Leu Asn
180 185 190

Pro Ser Ala Asp Asn Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr
195 200 205

Glu Glu Glu Ala Glu Asp Thr Thr Asp Glu Ala Glu Ile Pro Gly Thr
210 215 220

Pro Ser Ile Arg Gln Asn Ala Met Glu Thr Leu Thr Gly Leu Lys Ser
225 230 235 240

Ser Leu Leu Leu Gly Thr Lys Asp Asn Asn Thr Ile Ser Ala Glu Val
245 250 255

Asp Ser Leu Leu Ala Leu Leu Lys Glu Ser Gln Pro Ala Pro Ile Gln
260 265 270

Gly Pro Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr
275 280 285

Pro Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His
290 295 300

Glu Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp
305 310 315 320

Glu Ser Gly Phe Val Met Ser Tyr Phe Phe Lys Lys Asp Leu Thr Glu
325 330 335

Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu Glu Val Lys Thr Ser
340 345 350

His Asn Gly Leu Asp Ser Leu Ser Ser His Glu Gln Asp Tyr Pro Gly
355 360 365

Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys Ile Glu Glu Lys Ile
370 375 380

Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg Glu Ser Ile Val Val

385

390

395

400

Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro His Gly Asp His His His
 405 410 415

Ala Asp Pro Ile Asp Glu His Lys Pro Val Gly Ile Gly His Ser His
 420 425 430

Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly Val Ala Lys Lys Glu
 435 440 445

Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr Asn Val Val Asn Leu
 450 455 460

Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe Thr Leu Ala Asn Gly
 465 470 475 480

Gln Lys Arg Val Ser Phe Ser Phe Pro Pro Glu Leu Glu Lys Lys Leu
 485 490 495

Gly Ile Asn Met Leu Val Lys Leu Ile Thr Pro Asp Gly Lys Val Leu
 500 505 510

Glu Lys Val Ser Gly Lys Val Phe Gly Glu Gly Val Gly Asn Ile Ala
 515 520 525

Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly Gln Thr Phe Lys Tyr
 530 535 540

Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser Tyr Asp Gly Thr Phe
 545 550 555 560

Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala Ser Gln Thr Ile Phe
 565 570 575

Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg Val Asn Pro Gln Phe
 580 585 590

Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg Val Phe Asp Glu Phe
 595 600 605

His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys Val Gly Glu Ile Lys
 610 615 620

Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr Arg Thr Ala Gly Asn
625 630 635 640

Lys Ile Pro Val Thr Phe Met Ala Asn Ala Tyr Leu Asp Asn Gln Ser
645 650 655

Thr Tyr Ile Val Glu Val Pro Ile Leu Glu Lys Glu Asn Gln Thr Asp
660 665 670

Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn Lys Ala Gln Glu Asn
675 680 685

Ser Lys Leu Asp Glu Lys Val Glu Glu Pro Lys Thr Ser Glu Lys Val
690 695 700

Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser Thr Ser Asn Ser Thr
705 710 715 720

Leu Glu Glu Val Pro Thr Val Asp Pro Val Gln Glu Lys Val Ala Lys
725 730 735

Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn Val Leu Phe Asn Met
740 745 750

Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly Glu Val Ile Lys Lys
755 760 765

Asn Met Ala Asp Phe Thr Gly Glu Ala Pro Gln Gly Asn Gly Glu Asn
770 775 780

Lys Pro Ser Glu Asn Gly Lys Val Ser Thr Gly Thr Val Glu Asn Gln
785 790 795 800

Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro Glu Ala Pro Asn Glu
805 810 815

Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn Gly Met Leu Asn Pro
820 825 830

Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp Pro Ala Leu Glu Glu
835 840 845

Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu Glu Lys Phe Thr Ala
850 855 860

Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe Asn Met Asp Gly Thr
865 870 875 880

Ile Glu Leu Arg Leu Pro Ser Gly Glu Val Ile Lys Lys Asn Leu Ser
885 890 895

Asp Phe Ile Ala
900

<210> 336

<211> 894

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 336

Met Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
1 5 10 15

Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Thr Ser Trp Ile
20 25 30

Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr
35 40 45

Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser
50 55 60

Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys
65 70 75 80

Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr
85 90 95

Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro Ser Tyr Asp His
100 105 110

Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala
115 120 125

Pro Lys Gly Tyr Ser Leu Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr
130 135 140

Val Glu Pro Arg Asn Ala Ser Asp His Val Arg Lys Asn Lys Ala Asp
145 150 155 160

Gln Asp Ser Lys Pro Asp Glu Asp Lys Glu His Asp Glu Val Ser Glu
165 170 175

Pro Thr His Pro Glu Ser Asp Glu Lys Glu Asn His Ala Gly Leu Asn
180 185 190

Pro Ser Ala Asp Asn Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr
195 200 205

Glu Glu Glu Ala Glu Asp Thr Thr Asp Glu Ala Glu Ile Pro Gly Thr
210 215 220

Pro Ser Ile Arg Gln Asn Ala Met Glu Thr Leu Thr Gly Leu Lys Ser
225 230 235 240

Ser Leu Leu Leu Gly Thr Lys Asp Asn Asn Thr Ile Ser Ala Glu Val
245 250 255

Asp Ser Leu Leu Ala Leu Leu Lys Glu Ser Gln Pro Ala Pro Ile Gln
260 265 270

Gly Pro Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr
275 280 285

Pro Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His
290 295 300

Glu Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp
305 310 315 320

Glu Ser Gly Phe Val Met Ser Tyr Phe Phe Lys Lys Asp Leu Thr Glu
325 330 335

Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu Glu Val Lys Thr Ser
340 345 350

His Asn Gly Leu Asp Ser Leu Ser Ser His Glu Gln Asp Tyr Pro Gly
355 360 365

Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys Ile Glu Glu Lys Ile
370 375 380

Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg Glu Ser Ile Val Val
385 390 395 400

Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro Ala Asp Pro Ile Asp Glu
405 410 415

His Lys Pro Val Gly Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe
420 425 430

Lys Pro Glu Glu Gly Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr
435 440 445

Gly Glu Glu Leu Thr Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe
450 455 460

Asn Asn Gln Asn Phe Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe
465 470 475 480

Ser Phe Pro Pro Glu Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val
485 490 495

Lys Leu Ile Thr Pro Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys
500 505 510

Val Phe Gly Glu Gly Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln
515 520 525

Pro Tyr Leu Pro Gly Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp
530 535 540

Tyr Pro Glu Val Ser Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu
545 550 555 560

Ala Tyr Lys Met Ala Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly
565 570 575

Asp Thr Tyr Leu Arg Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr
580 585 590

Asp Ala Leu Val Arg Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu
595 600 605

Glu Asn Asn Tyr Lys Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu
610 615 620

Asn Gln Gly Thr Thr Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe
625 630 635 640

Met Ala Asn Ala Tyr Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val
645 650 655

Pro Ile Leu Glu Lys Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro
660 665 670

Gln Phe Lys Arg Asn Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys
675 680 685

Val Glu Glu Pro Lys Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser
690 695 700

Glu Thr Gly Asn Ser Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr
705 710 715 720

Val Asp Pro Val Gln Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly
725 730 735

Met Lys Leu Glu Asn Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu
740 745 750

Tyr Leu Pro Ser Gly Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr
755 760 765

Gly Glu Ala Pro Gln Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly
770 775 780

Lys Val Ser Thr Gly Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro
785 790 795 800

Ala Asp Ser Leu Pro Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu

805

810

815

Asn Ser Thr Asp Asn Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser
 820 825 830

Asp Pro Met Leu Asp Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro
 835 840 845

Val Gln Glu Lys Leu Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu
 850 855 860

Asp Ser Val Ile Phe Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro
 865 870 875 880

Ser Gly Glu Val Ile Lys Lys Asn Leu Ser Asp Phe Ile Ala
 885 890

<210> 337

<211> 894

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 337

Met Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
 1 5 10 15

Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Thr Ser Trp Ile
 20 25 30

Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr
 35 40 45

Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser
 50 55 60

Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys
 65 70 75 80

Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr
 85 90 95

Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro Asn Ile Lys Phe
100 105 110

Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala Pro Lys Gly Tyr Ser Leu
115 120 125

Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr Val Glu Pro Arg Asn Ala
130 135 140

Ser Asp His Val Arg Lys Asn Lys Ala Asp Gln Asp Ser Lys Pro Asp
145 150 155 160

Glu Asp Lys Glu His Asp Glu Val Ser Glu Pro Thr His Pro Glu Ser
165 170 175

Asp Glu Lys Glu Asn His Ala Gly Leu Asn Pro Ser Ala Asp Asn Leu
180 185 190

Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr Glu Glu Glu Ala Glu Asp
195 200 205

Thr Thr Asp Glu Ala Glu Ile Pro Gly Thr Pro Ser Ile Arg Gln Asn
210 215 220

Ala Met Glu Thr Leu Thr Gly Leu Lys Ser Ser Leu Leu Leu Gly Thr
225 230 235 240

Lys Asp Asn Asn Thr Ile Ser Ala Glu Val Asp Ser Leu Leu Ala Leu
245 250 255

Leu Lys Glu Ser Gln Pro Ala Pro Ile Gln Gly Pro Gln Ile Gly Gln
260 265 270

Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr Pro Ser Pro Ser Leu Pro
275 280 285

Ile Asn Pro Gly Thr Ser His Glu Lys His Glu Glu Asp Gly Tyr Gly
290 295 300

Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp Glu Ser Gly Phe Val Met
305 310 315 320

Ser Tyr Phe Phe Lys Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala

325

330

335

Gln Lys His Leu Glu Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser
 340 345 350

Leu Ser Ser His Glu Gln Asp Tyr Pro Gly Asn Ala Lys Glu Met Lys
 355 360 365

Asp Leu Asp Lys Lys Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln
 370 375 380

Tyr Gly Val Lys Arg Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala
 385 390 395 400

Ile Ile Tyr Pro His Gly Asp His His His Ala Asp Pro Ile Asp Glu
 405 410 415

His Lys Pro Val Gly Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe
 420 425 430

Lys Pro Glu Glu Gly Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr
 435 440 445

Gly Glu Glu Leu Thr Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe
 450 455 460

Asn Asn Gln Asn Phe Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe
 465 470 475 480

Ser Phe Pro Pro Glu Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val
 485 490 495

Lys Leu Ile Thr Pro Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys
 500 505 510

Val Phe Gly Glu Gly Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln
 515 520 525

Pro Tyr Leu Pro Gly Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp
 530 535 540

Tyr Pro Glu Val Ser Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu
 545 550 555 560

Ala Tyr Lys Met Ala Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly
565 570 575

Asp Thr Tyr Leu Arg Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr
580 585 590

Asp Ala Leu Val Arg Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu
595 600 605

Glu Asn Asn Tyr Lys Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu
610 615 620

Asn Gln Gly Thr Thr Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe
625 630 635 640

Met Ala Asn Ala Tyr Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val
645 650 655

Pro Ile Leu Glu Lys Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro
660 665 670

Gln Phe Lys Arg Asn Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys
675 680 685

Val Glu Glu Pro Lys Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser
690 695 700

Glu Thr Gly Asn Ser Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr
705 710 715 720

Val Asp Pro Val Gln Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly
725 730 735

Met Lys Leu Glu Asn Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu
740 745 750

Tyr Leu Pro Ser Gly Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr
755 760 765

Gly Glu Ala Pro Gln Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly
770 775 780

Lys Val Ser Thr Gly Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro
785 790 795 800

Ala Asp Ser Leu Pro Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu
805 810 815

Asn Ser Thr Asp Asn Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser
820 825 830

Asp Pro Met Leu Asp Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro
835 840 845

Val Gln Glu Lys Leu Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu
850 855 860

Asp Ser Val Ile Phe Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro
865 870 875 880

Ser Gly Glu Val Ile Lys Lys Asn Leu Ser Asp Phe Ile Ala
885 890

<210> 338

<211> 888

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 338

Met Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
1 5 10 15

Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Thr Ser Trp Ile
20 25 30

Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr
35 40 45

Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser
50 55 60

Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys
65 70 75 80

Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr
85 90 95

Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro Asn Ile Lys Phe
100 105 110

Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala Pro Lys Gly Tyr Ser Leu
115 120 125

Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr Val Glu Pro Arg Asn Ala
130 135 140

Ser Asp His Val Arg Lys Asn Lys Ala Asp Gln Asp Ser Lys Pro Asp
145 150 155 160

Glu Asp Lys Glu His Asp Glu Val Ser Glu Pro Thr His Pro Glu Ser
165 170 175

Asp Glu Lys Glu Asn His Ala Gly Leu Asn Pro Ser Ala Asp Asn Leu
180 185 190

Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr Glu Glu Glu Ala Glu Asp
195 200 205

Thr Thr Asp Glu Ala Glu Ile Pro Gly Thr Pro Ser Ile Arg Gln Asn
210 215 220

Ala Met Glu Thr Leu Thr Gly Leu Lys Ser Ser Leu Leu Leu Gly Thr
225 230 235 240

Lys Asp Asn Asn Thr Ile Ser Ala Glu Val Asp Ser Leu Leu Ala Leu
245 250 255

Leu Lys Glu Ser Gln Pro Ala Pro Ile Gln Gly Pro Gln Ile Gly Gln
260 265 270

Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr Pro Ser Pro Ser Leu Pro
275 280 285

Ile Asn Pro Gly Thr Ser His Glu Lys His Glu Glu Asp Gly Tyr Gly
290 295 300

Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp Glu Ser Gly Phe Val Met
305 310 315 320

Ser Tyr Phe Phe Lys Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala
325 330 335

Gln Lys His Leu Glu Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser
340 345 350

Leu Ser Ser His Glu Gln Asp Tyr Pro Gly Asn Ala Lys Glu Met Lys
355 360 365

Asp Leu Asp Lys Lys Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln
370 375 380

Tyr Gly Val Lys Arg Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala
385 390 395 400

Ile Ile Tyr Pro Ala Asp Pro Ile Asp Glu His Lys Pro Val Gly Ile
405 410 415

Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly Val
420 425 430

Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr Asn
435 440 445

Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe Thr
450 455 460

Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro Glu Leu
465 470 475 480

Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr Pro Asp
485 490 495

Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu Gly Val
500 505 510

Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly Gln
515 520 525

Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser Tyr
530 535 540

Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala Ser
545 550 555 560

Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg Val
565 570 575

Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg Val
580 585 590

Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys Val
595 600 605

Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr Arg
610 615 620

Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala Tyr Leu
625 630 635 640

Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu Glu Lys Glu
645 650 655

Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn Lys
660 665 670

Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys Val Glu Glu Pro Lys Thr
675 680 685

Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser Thr
690 695 700

Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro Val Gln Glu
705 710 715 720

Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn Val
725 730 735

Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly Glu
740 745 750

Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala Pro Gln Gly

755

760

765

Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser Thr Gly Thr
 770 775 780

Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro Glu
 785 790 795 800

Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn Gly
 805 810 815

Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp Pro
 820 825 830

Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu Glu
 835 840 845

Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe Asn
 850 855 860

Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val Ile Lys
 865 870 875 880

Lys Asn Leu Ser Asp Phe Ile Ala
 885

<210> 339

<211> 900

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism.

<400> 339

Met Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
 1 5 10 15

Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Thr Ser Trp Ile
 20 25 30

Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr
 35 40 45

Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser
50 55 60

Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys
65 70 75 80

Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr
85 90 95

Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro Ser Tyr Asp Ser
100 105 110

Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala
115 120 125

Pro Lys Gly Tyr Ser Leu Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr
130 135 140

Val Glu Pro Arg Asn Ala Ser Asp His Val Arg Lys Asn Lys Ala Asp
145 150 155 160

Gln Asp Ser Lys Pro Asp Glu Asp Lys Glu His Asp Glu Val Ser Glu
165 170 175

Pro Thr His Pro Glu Ser Asp Glu Lys Glu Asn His Ala Gly Leu Asn
180 185 190

Pro Ser Ala Asp Asn Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr
195 200 205

Glu Glu Glu Ala Glu Asp Thr Thr Asp Glu Ala Glu Ile Pro Gly Thr
210 215 220

Pro Ser Ile Arg Gln Asn Ala Met Glu Thr Leu Thr Gly Leu Lys Ser
225 230 235 240

Ser Leu Leu Leu Gly Thr Lys Asp Asn Asn Thr Ile Ser Ala Glu Val
245 250 255

Asp Ser Leu Leu Ala Leu Leu Lys Glu Ser Gln Pro Ala Pro Ile Gln
260 265 270

Gly Pro Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr

275

280

285

Pro Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His
 290 295 300

Glu Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp
 305 310 315 320

Glu Ser Gly Phe Val Met Ser Tyr Phe Phe Lys Lys Asp Leu Thr Glu
 325 330 335

Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu Glu Val Lys Thr Ser
 340 345 350

His Asn Gly Leu Asp Ser Leu Ser Ser His Glu Gln Asp Tyr Pro Gly
 355 360 365

Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys Ile Glu Glu Lys Ile
 370 375 380

Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg Glu Ser Ile Val Val
 385 390 395 400

Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro His Gly Asp His His His
 405 410 415

Ala Asp Pro Ile Asp Glu His Lys Pro Val Gly Ile Gly His Ser His
 420 425 430

Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly Val Ala Lys Lys Glu
 435 440 445

Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr Asn Val Val Asn Leu
 450 455 460

Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe Thr Leu Ala Asn Gly
 465 470 475 480

Gln Lys Arg Val Ser Phe Ser Phe Pro Pro Glu Leu Glu Lys Lys Leu
 485 490 495

Gly Ile Asn Met Leu Val Lys Leu Ile Thr Pro Asp Gly Lys Val Leu
 500 505 510

Glu Lys Val Ser Gly Lys Val Phe Gly Glu Gly Val Gly Asn Ile Ala
515 520 525

Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly Gln Thr Phe Lys Tyr
530 535 540

Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser Tyr Asp Gly Thr Phe
545 550 555 560

Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala Ser Gln Thr Ile Phe
565 570 575

Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg Val Asn Pro Gln Phe
580 585 590

Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg Val Phe Asp Glu Phe
595 600 605

His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys Val Gly Glu Ile Lys
610 615 620

Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr Arg Thr Ala Gly Asn
625 630 635 640

Lys Ile Pro Val Thr Phe Met Ala Asn Ala Tyr Leu Asp Asn Gln Ser
645 650 655

Thr Tyr Ile Val Glu Val Pro Ile Leu Glu Lys Glu Asn Gln Thr Asp
660 665 670

Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn Lys Ala Gln Glu Asn
675 680 685

Ser Lys Leu Asp Glu Lys Val Glu Glu Pro Lys Thr Ser Glu Lys Val
690 695 700

Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser Thr Ser Asn Ser Thr
705 710 715 720

Leu Glu Glu Val Pro Thr Val Asp Pro Val Gln Glu Lys Val Ala Lys
725 730 735

Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn Val Leu Phe Asn Met
740 745 750

Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly Glu Val Ile Lys Lys
755 760 765

Asn Met Ala Asp Phe Thr Gly Glu Ala Pro Gln Gly Asn Gly Glu Asn
770 775 780

Lys Pro Ser Glu Asn Gly Lys Val Ser Thr Gly Thr Val Glu Asn Gln
785 790 795 800

Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro Glu Ala Pro Asn Glu
805 810 815

Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn Gly Met Leu Asn Pro
820 825 830

Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp Pro Ala Leu Glu Glu
835 840 845

Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu Glu Lys Phe Thr Ala
850 855 860

Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe Asn Met Asp Gly Thr
865 870 875 880

Ile Glu Leu Arg Leu Pro Ser Gly Glu Val Ile Lys Lys Asn Leu Ser
885 890 895

Asp Phe Ile Ala
900

<210> 340
<211> 894
<212> PRT
<213> Artificial Sequence

<220>
<223> Unknown Organism

<400> 340

Met Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
1 5 10 15

Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Thr Ser Trp Ile
20 25 30

Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr
35 40 45

Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser
50 55 60

Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys
65 70 75 80

Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr
85 90 95

Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro Ser Tyr Asp Ser
100 105 110

Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala
115 120 125

Pro Lys Gly Tyr Ser Leu Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr
130 135 140

Val Glu Pro Arg Asn Ala Ser Asp His Val Arg Lys Asn Lys Ala Asp
145 150 155 160

Gln Asp Ser Lys Pro Asp Glu Asp Lys Glu His Asp Glu Val Ser Glu
165 170 175

Pro Thr His Pro Glu Ser Asp Glu Lys Glu Asn His Ala Gly Leu Asn
180 185 190

Pro Ser Ala Asp Asn Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr
195 200 205

Glu Glu Glu Ala Glu Asp Thr Thr Asp Glu Ala Glu Ile Pro Gly Thr
210 215 220

Pro Ser Ile Arg Gln Asn Ala Met Glu Thr Leu Thr Gly Leu Lys Ser
225 230 235 240

Ser Leu Leu Leu Gly Thr Lys Asp Asn Asn Thr Ile Ser Ala Glu Val
245 250 255

Asp Ser Leu Leu Ala Leu Leu Lys Glu Ser Gln Pro Ala Pro Ile Gln
260 265 270

Gly Pro Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr
275 280 285

Pro Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His
290 295 300

Glu Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp
305 310 315 320

Glu Ser Gly Phe Val Met Ser Tyr Phe Phe Lys Lys Asp Leu Thr Glu
325 330 335

Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu Glu Val Lys Thr Ser
340 345 350

His Asn Gly Leu Asp Ser Leu Ser Ser His Glu Gln Asp Tyr Pro Gly
355 360 365

Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys Ile Glu Glu Lys Ile
370 375 380

Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg Glu Ser Ile Val Val
385 390 395 400

Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro Ala Asp Pro Ile Asp Glu
405 410 415

His Lys Pro Val Gly Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe
420 425 430

Lys Pro Glu Glu Gly Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr
435 440 445

Gly Glu Glu Leu Thr Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe
450 455 460

Asn Asn Gln Asn Phe Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe
465 470 475 480

Ser Phe Pro Pro Glu Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val
485 490 495

Lys Leu Ile Thr Pro Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys
500 505 510

Val Phe Gly Glu Gly Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln
515 520 525

Pro Tyr Leu Pro Gly Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp
530 535 540

Tyr Pro Glu Val Ser Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu
545 550 555 560

Ala Tyr Lys Met Ala Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly
565 570 575

Asp Thr Tyr Leu Arg Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr
580 585 590

Asp Ala Leu Val Arg Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu
595 600 605

Glu Asn Asn Tyr Lys Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu
610 615 620

Asn Gln Gly Thr Thr Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe
625 630 635 640

Met Ala Asn Ala Tyr Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val
645 650 655

Pro Ile Leu Glu Lys Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro
660 665 670

Gln Phe Lys Arg Asn Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys
675 680 685

Val Glu Glu Pro Lys Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser

690

695

700

Glu Thr Gly Asn Ser Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr
 705 710 715 720

Val Asp Pro Val Gln Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly
 725 730 735

Met Lys Leu Glu Asn Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu
 740 745 750

Tyr Leu Pro Ser Gly Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr
 755 760 765

Gly Glu Ala Pro Gln Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly
 770 775 780

Lys Val Ser Thr Gly Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro
 785 790 795 800

Ala Asp Ser Leu Pro Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu
 805 810 815

Asn Ser Thr Asp Asn Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser
 820 825 830

Asp Pro Met Leu Asp Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro
 835 840 845

Val Gln Glu Lys Leu Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu
 850 855 860

Asp Ser Val Ile Phe Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro
 865 870 875 880

Ser Gly Glu Val Ile Lys Lys Asn Leu Ser Asp Phe Ile Ala
 885 890

<210> 341

<211> 900

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 341

Met Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
1 5 10 15

Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Thr Ser Trp Ile
20 25 30

Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr
35 40 45

Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser
50 55 60

Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys
65 70 75 80

Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr
85 90 95

Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro Ser Tyr Asp His
100 105 110

Tyr Ser Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala
115 120 125

Pro Lys Gly Tyr Ser Leu Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr
130 135 140

Val Glu Pro Arg Asn Ala Ser Asp His Val Arg Lys Asn Lys Ala Asp
145 150 155 160

Gln Asp Ser Lys Pro Asp Glu Asp Lys Glu His Asp Glu Val Ser Glu
165 170 175

Pro Thr His Pro Glu Ser Asp Glu Lys Glu Asn His Ala Gly Leu Asn
180 185 190

Pro Ser Ala Asp Asn Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr
195 200 205

Glu Glu Glu Ala Glu Asp Thr Thr Asp Glu Ala Glu Ile Pro Gly Thr

210

215

220

Pro Ser Ile Arg Gln Asn Ala Met Glu Thr Leu Thr Gly Leu Lys Ser
 225 230 235 240

Ser Leu Leu Leu Gly Thr Lys Asp Asn Asn Thr Ile Ser Ala Glu Val
 245 250 255

Asp Ser Leu Leu Ala Leu Leu Lys Glu Ser Gln Pro Ala Pro Ile Gln
 260 265 270

Gly Pro Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr
 275 280 285

Pro Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His
 290 295 300

Glu Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp
 305 310 315 320

Glu Ser Gly Phe Val Met Ser Tyr Phe Phe Lys Lys Asp Leu Thr Glu
 325 330 335

Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu Glu Val Lys Thr Ser
 340 345 350

His Asn Gly Leu Asp Ser Leu Ser Ser His Glu Gln Asp Tyr Pro Gly
 355 360 365

Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys Ile Glu Glu Lys Ile
 370 375 380

Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg Glu Ser Ile Val Val
 385 390 395 400

Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro His Gly Asp His His His
 405 410 415

Ala Asp Pro Ile Asp Glu His Lys Pro Val Gly Ile Gly His Ser His
 420 425 430

Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly Val Ala Lys Lys Glu
 435 440 445

Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr Asn Val Val Asn Leu
 450 455 460

Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe Thr Leu Ala Asn Gly
 465 470 475 480

Gln Lys Arg Val Ser Phe Ser Phe Pro Pro Glu Leu Glu Lys Lys Leu
 485 490 495

Gly Ile Asn Met Leu Val Lys Leu Ile Thr Pro Asp Gly Lys Val Leu
 500 505 510

Glu Lys Val Ser Gly Lys Val Phe Gly Glu Gly Val Gly Asn Ile Ala
 515 520 525

Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly Gln Thr Phe Lys Tyr
 530 535 540

Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser Tyr Asp Gly Thr Phe
 545 550 555 560

Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala Ser Gln Thr Ile Phe
 565 570 575

Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg Val Asn Pro Gln Phe
 580 585 590

Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg Val Phe Asp Glu Phe
 595 600 605

His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys Val Gly Glu Ile Lys
 610 615 620

Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr Arg Thr Ala Gly Asn
 625 630 635 640

Lys Ile Pro Val Thr Phe Met Ala Asn Ala Tyr Leu Asp Asn Gln Ser
 645 650 655

Thr Tyr Ile Val Glu Val Pro Ile Leu Glu Lys Glu Asn Gln Thr Asp
 660 665 670

Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn Lys Ala Gln Glu Asn
675 680 685

Ser Lys Leu Asp Glu Lys Val Glu Glu Pro Lys Thr Ser Glu Lys Val
690 695 700

Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser Thr Ser Asn Ser Thr
705 710 715 720

Leu Glu Glu Val Pro Thr Val Asp Pro Val Gln Glu Lys Val Ala Lys
725 730 735

Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn Val Leu Phe Asn Met
740 745 750

Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly Glu Val Ile Lys Lys
755 760 765

Asn Met Ala Asp Phe Thr Gly Glu Ala Pro Gln Gly Asn Gly Glu Asn
770 775 780

Lys Pro Ser Glu Asn Gly Lys Val Ser Thr Gly Thr Val Glu Asn Gln
785 790 795 800

Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro Glu Ala Pro Asn Glu
805 810 815

Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn Gly Met Leu Asn Pro
820 825 830

Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp Pro Ala Leu Glu Glu
835 840 845

Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu Glu Lys Phe Thr Ala
850 855 860

Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe Asn Met Asp Gly Thr
865 870 875 880

Ile Glu Leu Arg Leu Pro Ser Gly Glu Val Ile Lys Lys Asn Leu Ser
885 890 895

Asp Phe Ile Ala
900

<210> 342
<211> 894
<212> PRT
<213> Artificial Sequence

<220>
<223> Unknown Organism

<400> 342

Met Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
1 5 10 15

Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Thr Ser Trp Ile
20 25 30

Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr
35 40 45

Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser
50 55 60

Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys
65 70 75 80

Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr
85 90 95

Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro Ser Tyr Asp His
100 105 110

Tyr Ser Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala
115 120 125

Pro Lys Gly Tyr Ser Leu Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr
130 135 140

Val Glu Pro Arg Asn Ala Ser Asp His Val Arg Lys Asn Lys Ala Asp
145 150 155 160

Gln Asp Ser Lys Pro Asp Glu Asp Lys Glu His Asp Glu Val Ser Glu
165 170 175

Pro Thr His Pro Glu Ser Asp Glu Lys Glu Asn His Ala Gly Leu Asn
180 185 190

Pro Ser Ala Asp Asn Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr
195 200 205

Glu Glu Glu Ala Glu Asp Thr Thr Asp Glu Ala Glu Ile Pro Gly Thr
210 215 220

Pro Ser Ile Arg Gln Asn Ala Met Glu Thr Leu Thr Gly Leu Lys Ser
225 230 235 240

Ser Leu Leu Leu Gly Thr Lys Asp Asn Asn Thr Ile Ser Ala Glu Val
245 250 255

Asp Ser Leu Leu Ala Leu Leu Lys Glu Ser Gln Pro Ala Pro Ile Gln
260 265 270

Gly Pro Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr
275 280 285

Pro Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His
290 295 300

Glu Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp
305 310 315 320

Glu Ser Gly Phe Val Met Ser Tyr Phe Phe Lys Lys Asp Leu Thr Glu
325 330 335

Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu Glu Val Lys Thr Ser
340 345 350

His Asn Gly Leu Asp Ser Leu Ser Ser His Glu Gln Asp Tyr Pro Gly
355 360 365

Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys Ile Glu Glu Lys Ile
370 375 380

Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg Glu Ser Ile Val Val
385 390 395 400

Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro Ala Asp Pro Ile Asp Glu
405 410 415

His Lys Pro Val Gly Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe
420 425 430

Lys Pro Glu Glu Gly Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr
435 440 445

Gly Glu Glu Leu Thr Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe
450 455 460

Asn Asn Gln Asn Phe Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe
465 470 475 480

Ser Phe Pro Pro Glu Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val
485 490 495

Lys Leu Ile Thr Pro Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys
500 505 510

Val Phe Gly Glu Gly Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln
515 520 525

Pro Tyr Leu Pro Gly Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp
530 535 540

Tyr Pro Glu Val Ser Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu
545 550 555 560

Ala Tyr Lys Met Ala Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly
565 570 575

Asp Thr Tyr Leu Arg Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr
580 585 590

Asp Ala Leu Val Arg Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu
595 600 605

Glu Asn Asn Tyr Lys Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu
610 615 620

Asn Gln Gly Thr Thr Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe

625

630

635

640

Met Ala Asn Ala Tyr Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val
 645 650 655

Pro Ile Leu Glu Lys Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro
 660 665 670

Gln Phe Lys Arg Asn Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys
 675 680 685

Val Glu Glu Pro Lys Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser
 690 695 700

Glu Thr Gly Asn Ser Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr
 705 710 715 720

Val Asp Pro Val Gln Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly
 725 730 735

Met Lys Leu Glu Asn Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu
 740 745 750

Tyr Leu Pro Ser Gly Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr
 755 760 765

Gly Glu Ala Pro Gln Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly
 770 775 780

Lys Val Ser Thr Gly Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro
 785 790 795 800

Ala Asp Ser Leu Pro Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu
 805 810 815

Asn Ser Thr Asp Asn Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser
 820 825 830

Asp Pro Met Leu Asp Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro
 835 840 845

Val Gln Glu Lys Leu Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu
 850 855 860

Asp Ser Val Ile Phe Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro
865 870 875 880

Ser Gly Glu Val Ile Lys Lys Asn Leu Ser Asp Phe Ile Ala
885 890

<210> 343
<211> 901
<212> PRT
<213> Artificial Sequence

<220>
<223> Unknown Organism

<400> 343

Met Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
1 5 10 15

Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Thr Ser Trp Ile
20 25 30

Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr
35 40 45

Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser
50 55 60

Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys
65 70 75 80

Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr
85 90 95

Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro His Tyr Asp His
100 105 110

Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala
115 120 125

Pro Lys Gly Tyr Ser Leu Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr
130 135 140

Val Glu Pro Arg Asn Ala Ser Asp His Val Arg Lys Asn Lys Ala Asp

145	150	155	160
Gln Asp Ser Lys Pro Asp Glu Asp Lys Glu His Asp Glu Val Ser Glu	165	170	175
Pro Thr His Pro Glu Ser Asp Glu Lys Glu Asn His Ala Gly Leu Asn	180	185	190
Pro Ser Ala Asp Asn Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr	195	200	205
Glu Glu Glu Ala Glu Asp Thr Thr Asp Glu Ala Glu Ile Pro Gly Thr	210	215	220
Pro Ser Ile Arg Gln Asn Ala Met Glu Thr Leu Thr Gly Leu Lys Ser	225	230	235
Ser Leu Leu Leu Gly Thr Lys Asp Asn Asn Thr Ile Ser Ala Glu Val	245	250	255
Asp Ser Leu Leu Ala Leu Leu Lys Glu Ser Gln Pro Ala Pro Ile Gln	260	265	270
Ser Gly Pro Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala	275	280	285
Thr Pro Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys	290	295	300
His Glu Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu	305	310	315
Asp Glu Ser Gly Phe Val Met Ser Tyr Phe Phe Lys Lys Asp Leu Thr	325	330	335
Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu Glu Val Lys Thr	340	345	350
Ser His Asn Gly Leu Asp Ser Leu Ser Ser His Glu Gln Asp Tyr Pro	355	360	365
Gly Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys Ile Glu Glu Lys	370	375	380

Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg Glu Ser Ile Val
385 390 395 400

Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro His Gly Asp His His
405 410 415

His Ala Asp Pro Ile Asp Glu His Lys Pro Val Gly Ile Gly His Ser
420 425 430

His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly Val Ala Lys Lys
435 440 445

Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr Asn Val Val Asn
450 455 460

Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe Thr Leu Ala Asn
465 470 475 480

Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro Glu Leu Glu Lys Lys
485 490 495

Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr Pro Asp Gly Lys Val
500 505 510

Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu Gly Val Gly Asn Ile
515 520 525

Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly Gln Thr Phe Lys
530 535 540

Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser Tyr Asp Gly Thr
545 550 555 560

Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala Ser Gln Thr Ile
565 570 575

Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg Val Asn Pro Gln
580 585 590

Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg Val Phe Asp Glu
595 600 605

Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys Val Gly Glu Ile
610 615 620

Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr Arg Thr Ala Gly
625 630 635 640

Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala Tyr Leu Asp Asn Gln
645 650 655

Ser Thr Tyr Ile Val Glu Val Pro Ile Leu Glu Lys Glu Asn Gln Thr
660 665 670

Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn Lys Ala Gln Glu
675 680 685

Asn Ser Lys Leu Asp Glu Lys Val Glu Glu Pro Lys Thr Ser Glu Lys
690 695 700

Val Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser Thr Ser Asn Ser
705 710 715 720

Thr Leu Glu Glu Val Pro Thr Val Asp Pro Val Gln Glu Lys Val Ala
725 730 735

Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn Val Leu Phe Asn
740 745 750

Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly Glu Val Ile Lys
755 760 765

Lys Asn Met Ala Asp Phe Thr Gly Glu Ala Pro Gln Gly Asn Gly Glu
770 775 780

Asn Lys Pro Ser Glu Asn Gly Lys Val Ser Thr Gly Thr Val Glu Asn
785 790 795 800

Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro Glu Ala Pro Asn
805 810 815

Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn Gly Met Leu Asn
820 825 830

Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp Pro Ala Leu Glu
835 840 845

Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu Glu Lys Phe Thr
850 855 860

Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe Asn Met Asp Gly
865 870 875 880

Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val Ile Lys Lys Asn Leu
885 890 895

Ser Asp Phe Ile Ala
900

<210> 344
<211> 895
<212> PRT
<213> Artificial Sequence

<220>
<223> Unknown Organism

<400> 344

Met Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
1 5 10 15

Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Thr Ser Trp Ile
20 25 30

Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr
35 40 45

Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser
50 55 60

Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys
65 70 75 80

Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr
85 90 95

Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro His Tyr Asp His
100 105 110

Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala
115 120 125

Pro Lys Gly Tyr Ser Leu Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr
130 135 140

Val Glu Pro Arg Asn Ala Ser Asp His Val Arg Lys Asn Lys Ala Asp
145 150 155 160

Gln Asp Ser Lys Pro Asp Glu Asp Lys Glu His Asp Glu Val Ser Glu
165 170 175

Pro Thr His Pro Glu Ser Asp Glu Lys Glu Asn His Ala Gly Leu Asn
180 185 190

Pro Ser Ala Asp Asn Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr
195 200 205

Glu Glu Glu Ala Glu Asp Thr Thr Asp Glu Ala Glu Ile Pro Gly Thr
210 215 220

Pro Ser Ile Arg Gln Asn Ala Met Glu Thr Leu Thr Gly Leu Lys Ser
225 230 235 240

Ser Leu Leu Leu Gly Thr Lys Asp Asn Asn Thr Ile Ser Ala Glu Val
245 250 255

Asp Ser Leu Leu Ala Leu Leu Lys Glu Ser Gln Pro Ala Pro Ile Gln
260 265 270

Ser Gly Pro Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala
275 280 285

Thr Pro Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys
290 295 300

His Glu Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu
305 310 315 320

Asp Glu Ser Gly Phe Val Met Ser Tyr Phe Phe Lys Lys Asp Leu Thr
325 330 335

Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu Glu Val Lys Thr
 340 345 350

Ser His Asn Gly Leu Asp Ser Leu Ser Ser His Glu Gln Asp Tyr Pro
 355 360 365

Gly Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys Ile Glu Glu Lys
 370 375 380

Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg Glu Ser Ile Val
 385 390 395 400

Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro Ala Asp Pro Ile Asp
 405 410 415

Glu His Lys Pro Val Gly Ile Gly His Ser His Ser Asn Tyr Glu Leu
 420 425 430

Phe Lys Pro Glu Glu Gly Val Ala Lys Lys Glu Gly Asn Lys Val Tyr
 435 440 445

Thr Gly Glu Glu Leu Thr Asn Val Val Asn Leu Leu Lys Asn Ser Thr
 450 455 460

Phe Asn Asn Gln Asn Phe Thr Leu Ala Asn Gly Gln Lys Arg Val Ser
 465 470 475 480

Phe Ser Phe Pro Pro Glu Leu Glu Lys Lys Leu Gly Ile Asn Met Leu
 485 490 495

Val Lys Leu Ile Thr Pro Asp Gly Lys Val Leu Glu Lys Val Ser Gly
 500 505 510

Lys Val Phe Gly Glu Gly Val Gly Asn Ile Ala Asn Phe Glu Leu Asp
 515 520 525

Gln Pro Tyr Leu Pro Gly Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys
 530 535 540

Asp Tyr Pro Glu Val Ser Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser
 545 550 555 560

Leu Ala Tyr Lys Met Ala Ser Gln Thr Ile Phe Tyr Pro Phe His Ala

565

570

575

Gly Asp Thr Tyr Leu Arg Val Asn Pro Gln Phe Ala Val Pro Lys Gly
 580 585 590

Thr Asp Ala Leu Val Arg Val Phe Asp Glu Phe His Gly Asn Ala Tyr
 595 600 605

Leu Glu Asn Asn Tyr Lys Val Gly Glu Ile Lys Leu Pro Ile Pro Lys
 610 615 620

Leu Asn Gln Gly Thr Thr Arg Thr Ala Gly Asn Lys Ile Pro Val Thr
 625 630 635 640

Phe Met Ala Asn Ala Tyr Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu
 645 650 655

Val Pro Ile Leu Glu Lys Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu
 660 665 670

Pro Gln Phe Lys Arg Asn Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu
 675 680 685

Lys Val Glu Glu Pro Lys Thr Ser Glu Lys Val Glu Lys Glu Lys Leu
 690 695 700

Ser Glu Thr Gly Asn Ser Thr Ser Asn Ser Thr Leu Glu Glu Val Pro
 705 710 715 720

Thr Val Asp Pro Val Gln Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr
 725 730 735

Gly Met Lys Leu Glu Asn Val Leu Phe Asn Met Asp Gly Thr Ile Glu
 740 745 750

Leu Tyr Leu Pro Ser Gly Glu Val Ile Lys Lys Asn Met Ala Asp Phe
 755 760 765

Thr Gly Glu Ala Pro Gln Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn
 770 775 780

Gly Lys Val Ser Thr Gly Thr Val Glu Asn Gln Pro Thr Glu Asn Lys
 785 790 795 800

Pro Ala Asp Ser Leu Pro Glu Ala Pro Asn Glu Lys Pro Val Lys Pro
805 810 815

Glu Asn Ser Thr Asp Asn Gly Met Leu Asn Pro Glu Gly Asn Val Gly
820 825 830

Ser Asp Pro Met Leu Asp Pro Ala Leu Glu Glu Ala Pro Ala Val Asp
835 840 845

Pro Val Gln Glu Lys Leu Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly
850 855 860

Leu Asp Ser Val Ile Phe Asn Met Asp Gly Thr Ile Glu Leu Arg Leu
865 870 875 880

Pro Ser Gly Glu Val Ile Lys Lys Asn Leu Ser Asp Phe Ile Ala
885 890 895

<210> 345

<211> 901

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 345

Met Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
1 5 10 15

Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Thr Ser Trp Ile
20 25 30

Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr
35 40 45

Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser
50 55 60

Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys
65 70 75 80

Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr

85

90

95

Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro Ser Tyr Asp Ser
 100 105 110

Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala
 115 120 125

Pro Lys Gly Tyr Ser Leu Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr
 130 135 140

Val Glu Pro Arg Asn Ala Ser Asp His Val Arg Lys Asn Lys Ala Asp
 145 150 155 160

Gln Asp Ser Lys Pro Asp Glu Asp Lys Glu His Asp Glu Val Ser Glu
 165 170 175

Pro Thr His Pro Glu Ser Asp Glu Lys Glu Asn His Ala Gly Leu Asn
 180 185 190

Pro Ser Ala Asp Asn Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr
 195 200 205

Glu Glu Glu Ala Glu Asp Thr Thr Asp Glu Ala Glu Ile Pro Gly Thr
 210 215 220

Pro Ser Ile Arg Gln Asn Ala Met Glu Thr Leu Thr Gly Leu Lys Ser
 225 230 235 240

Ser Leu Leu Leu Gly Thr Lys Asp Asn Asn Thr Ile Ser Ala Glu Val
 245 250 255

Asp Ser Leu Leu Ala Leu Leu Lys Glu Ser Gln Pro Ala Pro Ile Gln
 260 265 270

Ser Gly Pro Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala
 275 280 285

Thr Pro Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys
 290 295 300

His Glu Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu
 305 310 315 320

Asp Glu Ser Gly Phe Val Met Ser Tyr Phe Phe Lys Lys Asp Leu Thr
325 330 335

Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu Glu Val Lys Thr
340 345 350

Ser His Asn Gly Leu Asp Ser Leu Ser Ser His Glu Gln Asp Tyr Pro
355 360 365

Gly Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys Ile Glu Glu Lys
370 375 380

Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg Glu Ser Ile Val
385 390 395 400

Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro His Gly Asp His His
405 410 415

His Ala Asp Pro Ile Asp Glu His Lys Pro Val Gly Ile Gly His Ser
420 425 430

His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly Val Ala Lys Lys
435 440 445

Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr Asn Val Val Asn
450 455 460

Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe Thr Leu Ala Asn
465 470 475 480

Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro Glu Leu Glu Lys Lys
485 490 495

Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr Pro Asp Gly Lys Val
500 505 510

Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu Gly Val Gly Asn Ile
515 520 525

Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly Gln Thr Phe Lys
530 535 540

Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser Tyr Asp Gly Thr
545 550 555 560

Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala Ser Gln Thr Ile
565 570 575

Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg Val Asn Pro Gln
580 585 590

Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg Val Phe Asp Glu
595 600 605

Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys Val Gly Glu Ile
610 615 620

Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr Arg Thr Ala Gly
625 630 635 640

Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala Tyr Leu Asp Asn Gln
645 650 655

Ser Thr Tyr Ile Val Glu Val Pro Ile Leu Glu Lys Glu Asn Gln Thr
660 665 670

Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn Lys Ala Gln Glu
675 680 685

Asn Ser Lys Leu Asp Glu Lys Val Glu Glu Pro Lys Thr Ser Glu Lys
690 695 700

Val Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser Thr Ser Asn Ser
705 710 715 720

Thr Leu Glu Glu Val Pro Thr Val Asp Pro Val Gln Glu Lys Val Ala
725 730 735

Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn Val Leu Phe Asn
740 745 750

Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly Glu Val Ile Lys
755 760 765

Lys Asn Met Ala Asp Phe Thr Gly Glu Ala Pro Gln Gly Asn Gly Glu
770 775 780

Asn Lys Pro Ser Glu Asn Gly Lys Val Ser Thr Gly Thr Val Glu Asn
785 790 795 800

Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro Glu Ala Pro Asn
805 810 815

Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn Gly Met Leu Asn
820 825 830

Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp Pro Ala Leu Glu
835 840 845

Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu Glu Lys Phe Thr
850 855 860

Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe Asn Met Asp Gly
865 870 875 880

Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val Ile Lys Lys Asn Leu
885 890 895

Ser Asp Phe Ile Ala
900

<210> 346

<211> 895

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 346

Met Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
1 5 10 15

Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Thr Ser Trp Ile
20 25 30

Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr
35 40 45

Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser
50 55 60

Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys
65 70 75 80

Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr
85 90 95

Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro Ser Tyr Asp Ser
100 105 110

Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala
115 120 125

Pro Lys Gly Tyr Ser Leu Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr
130 135 140

Val Glu Pro Arg Asn Ala Ser Asp His Val Arg Lys Asn Lys Ala Asp
145 150 155 160

Gln Asp Ser Lys Pro Asp Glu Asp Lys Glu His Asp Glu Val Ser Glu
165 170 175

Pro Thr His Pro Glu Ser Asp Glu Lys Glu Asn His Ala Gly Leu Asn
180 185 190

Pro Ser Ala Asp Asn Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr
195 200 205

Glu Glu Glu Ala Glu Asp Thr Thr Asp Glu Ala Glu Ile Pro Gly Thr
210 215 220

Pro Ser Ile Arg Gln Asn Ala Met Glu Thr Leu Thr Gly Leu Lys Ser
225 230 235 240

Ser Leu Leu Leu Gly Thr Lys Asp Asn Asn Thr Ile Ser Ala Glu Val
245 250 255

Asp Ser Leu Leu Ala Leu Leu Lys Glu Ser Gln Pro Ala Pro Ile Gln
260 265 270

Ser Gly Pro Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala
275 280 285

Thr Pro Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys
290 295 300

His Glu Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu
305 310 315 320

Asp Glu Ser Gly Phe Val Met Ser Tyr Phe Phe Lys Lys Asp Leu Thr
325 330 335

Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu Glu Val Lys Thr
340 345 350

Ser His Asn Gly Leu Asp Ser Leu Ser Ser His Glu Gln Asp Tyr Pro
355 360 365

Gly Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys Ile Glu Glu Lys
370 375 380

Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg Glu Ser Ile Val
385 390 395 400

Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro Ala Asp Pro Ile Asp
405 410 415

Glu His Lys Pro Val Gly Ile Gly His Ser His Ser Asn Tyr Glu Leu
420 425 430

Phe Lys Pro Glu Glu Gly Val Ala Lys Lys Glu Gly Asn Lys Val Tyr
435 440 445

Thr Gly Glu Glu Leu Thr Asn Val Val Asn Leu Leu Lys Asn Ser Thr
450 455 460

Phe Asn Asn Gln Asn Phe Thr Leu Ala Asn Gly Gln Lys Arg Val Ser
465 470 475 480

Phe Ser Phe Pro Pro Glu Leu Glu Lys Lys Leu Gly Ile Asn Met Leu
485 490 495

Val Lys Leu Ile Thr Pro Asp Gly Lys Val Leu Glu Lys Val Ser Gly

500

505

510

Lys Val Phe Gly Glu Gly Val Gly Asn Ile Ala Asn Phe Glu Leu Asp
 515 520 525

Gln Pro Tyr Leu Pro Gly Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys
 530 535 540

Asp Tyr Pro Glu Val Ser Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser
 545 550 555 560

Leu Ala Tyr Lys Met Ala Ser Gln Thr Ile Phe Tyr Pro Phe His Ala
 565 570 575

Gly Asp Thr Tyr Leu Arg Val Asn Pro Gln Phe Ala Val Pro Lys Gly
 580 585 590

Thr Asp Ala Leu Val Arg Val Phe Asp Glu Phe His Gly Asn Ala Tyr
 595 600 605

Leu Glu Asn Asn Tyr Lys Val Gly Glu Ile Lys Leu Pro Ile Pro Lys
 610 615 620

Leu Asn Gln Gly Thr Thr Arg Thr Ala Gly Asn Lys Ile Pro Val Thr
 625 630 635 640

Phe Met Ala Asn Ala Tyr Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu
 645 650 655

Val Pro Ile Leu Glu Lys Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu
 660 665 670

Pro Gln Phe Lys Arg Asn Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu
 675 680 685

Lys Val Glu Glu Pro Lys Thr Ser Glu Lys Val Glu Lys Glu Lys Leu
 690 695 700

Ser Glu Thr Gly Asn Ser Thr Ser Asn Ser Thr Leu Glu Glu Val Pro
 705 710 715 720

Thr Val Asp Pro Val Gln Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr
 725 730 735

Gly Met Lys Leu Glu Asn Val Leu Phe Asn Met Asp Gly Thr Ile Glu
740 745 750

Leu Tyr Leu Pro Ser Gly Glu Val Ile Lys Lys Asn Met Ala Asp Phe
755 760 765

Thr Gly Glu Ala Pro Gln Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn
770 775 780

Gly Lys Val Ser Thr Gly Thr Val Glu Asn Gln Pro Thr Glu Asn Lys
785 790 795 800

Pro Ala Asp Ser Leu Pro Glu Ala Pro Asn Glu Lys Pro Val Lys Pro
805 810 815

Glu Asn Ser Thr Asp Asn Gly Met Leu Asn Pro Glu Gly Asn Val Gly
820 825 830

Ser Asp Pro Met Leu Asp Pro Ala Leu Glu Glu Ala Pro Ala Val Asp
835 840 845

Pro Val Gln Glu Lys Leu Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly
850 855 860

Leu Asp Ser Val Ile Phe Asn Met Asp Gly Thr Ile Glu Leu Arg Leu
865 870 875 880

Pro Ser Gly Glu Val Ile Lys Lys Asn Leu Ser Asp Phe Ile Ala
885 890 895

<210> 347

<211> 895

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 347

Met Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
1 5 10 15

Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Thr Ser Trp Ile

20

25

30

Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr
 35 40 45

Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser
 50 55 60

Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys
 65 70 75 80

Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr
 85 90 95

Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro Asn Ile Lys Phe
 100 105 110

Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala Pro Lys Gly Tyr Ser Leu
 115 120 125

Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr Val Glu Pro Arg Asn Ala
 130 135 140

Ser Asp His Val Arg Lys Asn Lys Ala Asp Gln Asp Ser Lys Pro Asp
 145 150 155 160

Glu Asp Lys Glu His Asp Glu Val Ser Glu Pro Thr His Pro Glu Ser
 165 170 175

Asp Glu Lys Glu Asn His Ala Gly Leu Asn Pro Ser Ala Asp Asn Leu
 180 185 190

Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr Glu Glu Ala Glu Asp
 195 200 205

Thr Thr Asp Glu Ala Glu Ile Pro Gly Thr Pro Ser Ile Arg Gln Asn
 210 215 220

Ala Met Glu Thr Leu Thr Gly Leu Lys Ser Ser Leu Leu Leu Gly Thr
 225 230 235 240

Lys Asp Asn Asn Thr Ile Ser Ala Glu Val Asp Ser Leu Leu Ala Leu
 245 250 255

Phe Ser Phe Pro Pro Glu Leu Glu Lys Lys Leu Gly Ile Asn Met Leu
485 490 495

Val Lys Leu Ile Thr Pro Asp Gly Lys Val Leu Glu Lys Val Ser Gly
500 505 510

Lys Val Phe Gly Glu Gly Val Gly Asn Ile Ala Asn Phe Glu Leu Asp
515 520 525

Gln Pro Tyr Leu Pro Gly Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys
530 535 540

Asp Tyr Pro Glu Val Ser Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser
545 550 555 560

Leu Ala Tyr Lys Met Ala Ser Gln Thr Ile Phe Tyr Pro Phe His Ala
565 570 575

Gly Asp Thr Tyr Leu Arg Val Asn Pro Gln Phe Ala Val Pro Lys Gly
580 585 590

Thr Asp Ala Leu Val Arg Val Phe Asp Glu Phe His Gly Asn Ala Tyr
595 600 605

Leu Glu Asn Asn Tyr Lys Val Gly Glu Ile Lys Leu Pro Ile Pro Lys
610 615 620

Leu Asn Gln Gly Thr Thr Arg Thr Ala Gly Asn Lys Ile Pro Val Thr
625 630 635 640

Phe Met Ala Asn Ala Tyr Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu
645 650 655

Val Pro Ile Leu Glu Lys Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu
660 665 670

Pro Gln Phe Lys Arg Asn Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu
675 680 685

Lys Val Glu Glu Pro Lys Thr Ser Glu Lys Val Glu Lys Glu Lys Leu
690 695 700

Ser Glu Thr Gly Asn Ser Thr Ser Asn Ser Thr Leu Glu Glu Val Pro
705 710 715 720

Thr Val Asp Pro Val Gln Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr
725 730 735

Gly Met Lys Leu Glu Asn Val Leu Phe Asn Met Asp Gly Thr Ile Glu
740 745 750

Leu Tyr Leu Pro Ser Gly Glu Val Ile Lys Lys Asn Met Ala Asp Phe
755 760 765

Thr Gly Glu Ala Pro Gln Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn
770 775 780

Gly Lys Val Ser Thr Gly Thr Val Glu Asn Gln Pro Thr Glu Asn Lys
785 790 795 800

Pro Ala Asp Ser Leu Pro Glu Ala Pro Asn Glu Lys Pro Val Lys Pro
805 810 815

Glu Asn Ser Thr Asp Asn Gly Met Leu Asn Pro Glu Gly Asn Val Gly
820 825 830

Ser Asp Pro Met Leu Asp Pro Ala Leu Glu Glu Ala Pro Ala Val Asp
835 840 845

Pro Val Gln Glu Lys Leu Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly
850 855 860

Leu Asp Ser Val Ile Phe Asn Met Asp Gly Thr Ile Glu Leu Arg Leu
865 870 875 880

Pro Ser Gly Glu Val Ile Lys Lys Asn Leu Ser Asp Phe Ile Ala
885 890 895

<210> 348

<211> 889

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 348

Met Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
1 5 10 15

Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Thr Ser Trp Ile
20 25 30

Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr
35 40 45

Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser
50 55 60

Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys
65 70 75 80

Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr
85 90 95

Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro Asn Ile Lys Phe
100 105 110

Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala Pro Lys Gly Tyr Ser Leu
115 120 125

Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr Val Glu Pro Arg Asn Ala
130 135 140

Ser Asp His Val Arg Lys Asn Lys Ala Asp Gln Asp Ser Lys Pro Asp
145 150 155 160

Glu Asp Lys Glu His Asp Glu Val Ser Glu Pro Thr His Pro Glu Ser
165 170 175

Asp Glu Lys Glu Asn His Ala Gly Leu Asn Pro Ser Ala Asp Asn Leu
180 185 190

Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr Glu Glu Glu Ala Glu Asp
195 200 205

Thr Thr Asp Glu Ala Glu Ile Pro Gly Thr Pro Ser Ile Arg Gln Asn
210 215 220

Ala Met Glu Thr Leu Thr Gly Leu Lys Ser Ser Leu Leu Leu Gly Thr
225 230 235 240

Lys Asp Asn Asn Thr Ile Ser Ala Glu Val Asp Ser Leu Leu Ala Leu
245 250 255

Leu Lys Glu Ser Gln Pro Ala Pro Ile Gln Ser Gly Pro Gln Ile Gly
260 265 270

Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr Pro Ser Pro Ser Leu
275 280 285

Pro Ile Asn Pro Gly Thr Ser His Glu Lys His Glu Glu Asp Gly Tyr
290 295 300

Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp Glu Ser Gly Phe Val
305 310 315 320

Met Ser Tyr Phe Phe Lys Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala
325 330 335

Ala Gln Lys His Leu Glu Glu Val Lys Thr Ser His Asn Gly Leu Asp
340 345 350

Ser Leu Ser Ser His Glu Gln Asp Tyr Pro Gly Asn Ala Lys Glu Met
355 360 365

Lys Asp Leu Asp Lys Lys Ile Glu Glu Lys Ile Ala Gly Ile Met Lys
370 375 380

Gln Tyr Gly Val Lys Arg Glu Ser Ile Val Val Asn Lys Glu Lys Asn
385 390 395 400

Ala Ile Ile Tyr Pro Ala Asp Pro Ile Asp Glu His Lys Pro Val Gly
405 410 415

Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly
420 425 430

Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr
435 440 445

Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe

450

455

460

Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro Glu
 465 470 475 480

Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr Pro
 485 490 495

Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu Gly
 500 505 510

Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly
 515 520 525

Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser
 530 535 540

Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala
 545 550 555 560

Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg
 565 570 575

Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg
 580 585 590

Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys
 595 600 605

Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr
 610 615 620

Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala Tyr
 625 630 635 640

Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu Glu Lys
 645 650 655

Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn
 660 665 670

Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys Val Glu Glu Pro Lys
 675 680 685

Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser
690 695 700

Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro Val Gln
705 710 715 720

Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn
725 730 735

Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly
740 745 750

Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala Pro Gln
755 760 765

Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser Thr Gly
770 775 780

Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro
785 790 795 800

Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn
805 810 815

Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp
820 825 830

Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu
835 840 845

Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe
850 855 860

Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val Ile
865 870 875 880

Lys Lys Asn Leu Ser Asp Phe Ile Ala
885

<210> 349

<211> 633

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 349

Met Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr Pro
1 5 10 15

Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His Glu
20 25 30

Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp Glu
35 40 45

Ser Gly Phe Val Met Ser Ser Gly Asp Ser Asn Ser Tyr Phe Phe Lys
50 55 60

Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu
65 70 75 80

Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser His Glu
85 90 95

Gln Asp Tyr Pro Gly Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys
100 105 110

Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg
115 120 125

Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro Ser
130 135 140

Gly Asp Gly Thr Ser Ala Asp Pro Ile Asp Glu His Lys Pro Val Gly
145 150 155 160

Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly
165 170 175

Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr
180 185 190

Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe
195 200 205

Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro Glu
 210 215 220

Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr Pro
 225 230 235 240

Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu Gly
 245 250 255

Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly
 260 265 270

Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser
 275 280 285

Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala
 290 295 300

Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg
 305 310 315 320

Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg
 325 330 335

Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys
 340 345 350

Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr
 355 360 365

Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala Tyr
 370 375 380

Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu Glu Lys
 385 390 395 400

Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn
 405 410 415

Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys Val Glu Glu Pro Lys
 420 425 430

Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser
435 440 445

Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro Val Gln
450 455 460

Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn
465 470 475 480

Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly
485 490 495

Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala Pro Gln
500 505 510

Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser Thr Gly
515 520 525

Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro
530 535 540

Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn
545 550 555 560

Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp
565 570 575

Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu
580 585 590

Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe
595 600 605

Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val Ile
610 615 620

Lys Lys Asn Leu Ser Asp Phe Ile Ala
625 630

<210> 350

<211> 633

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 350

Met Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr Pro
1 5 10 15

Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His Glu
20 25 30

Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp Glu
35 40 45

Ser Gly Phe Val Met Ser Ser Gly Asp His Asn His Tyr Phe Phe Lys
50 55 60

Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu
65 70 75 80

Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser His Glu
85 90 95

Gln Asp Tyr Pro Gly Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys
100 105 110

Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg
115 120 125

Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro His
130 135 140

Gly Asp His His His Ala Asp Pro Ile Asp Glu His Lys Pro Val Gly
145 150 155 160

Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly
165 170 175

Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr
180 185 190

Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe
195 200 205

Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro Glu
210 215 220

Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr Pro
225 230 235 240

Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu Gly
245 250 255

Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly
260 265 270

Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser
275 280 285

Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala
290 295 300

Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg
305 310 315 320

Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg
325 330 335

Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys
340 345 350

Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr
355 360 365

Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala Tyr
370 375 380

Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu Glu Lys
385 390 395 400

Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn
405 410 415

Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys Val Glu Glu Pro Lys
420 425 430

Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser
435 440 445

Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro Val Gln
450 455 460

Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn
465 470 475 480

Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly
485 490 495

Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala Pro Gln
500 505 510

Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser Thr Gly
515 520 525

Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro
530 535 540

Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn
545 550 555 560

Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp
565 570 575

Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu
580 585 590

Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe
595 600 605

Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val Ile
610 615 620

Lys Lys Asn Leu Ser Asp Phe Ile Ala
625 630

<210> 351

<211> 633

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 351

Met Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr Pro
1 5 10 15

Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His Glu
20 25 30

Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp Glu
35 40 45

Ser Gly Phe Val Met Ser Ser Gly Asp Ser Asn His Tyr Phe Phe Lys
50 55 60

Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu
65 70 75 80

Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser His Glu
85 90 95

Gln Asp Tyr Pro Gly Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys
100 105 110

Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg
115 120 125

Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro His
130 135 140

Gly Asp His His His Ala Asp Pro Ile Asp Glu His Lys Pro Val Gly
145 150 155 160

Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly
165 170 175

Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr
180 185 190

Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe
195 200 205

Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro Glu
210 215 220

Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr Pro
225 230 235 240

Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu Gly
245 250 255

Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly
260 265 270

Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser
275 280 285

Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala
290 295 300

Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg
305 310 315 320

Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg
325 330 335

Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys
340 345 350

Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr
355 360 365

Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala Tyr
370 375 380

Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu Glu Lys
385 390 395 400

Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn
405 410 415

Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys Val Glu Glu Pro Lys
420 425 430

Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser

435

440

445

Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro Val Gln
 450 455 460

Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn
 465 470 475 480

Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly
 485 490 495

Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala Pro Gln
 500 505 510

Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser Thr Gly
 515 520 525

Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro
 530 535 540

Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn
 545 550 555 560

Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp
 565 570 575

Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu
 580 585 590

Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe
 595 600 605

Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val Ile
 610 615 620

Lys Lys Asn Leu Ser Asp Phe Ile Ala
 625 630

<210> 352

<211> 633

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 352

Met Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr Pro
1 5 10 15

Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His Glu
20 25 30

Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp Glu
35 40 45

Ser Gly Phe Val Met Ser Ser Gly Asp His Asn His Tyr Phe Phe Lys
50 55 60

Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu
65 70 75 80

Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser His Glu
85 90 95

Gln Asp Tyr Pro Gly Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys
100 105 110

Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg
115 120 125

Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro Ser
130 135 140

Gly Asp His His His Ala Asp Pro Ile Asp Glu His Lys Pro Val Gly
145 150 155 160

Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly
165 170 175

Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr
180 185 190

Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe
195 200 205

Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro Glu

210

215

220

Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr Pro
 225 230 235 240

Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu Gly
 245 250 255

Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly
 260 265 270

Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser
 275 280 285

Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala
 290 295 300

Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg
 305 310 315 320

Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg
 325 330 335

Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys
 340 345 350

Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr
 355 360 365

Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala Tyr
 370 375 380

Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu Glu Lys
 385 390 395 400

Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn
 405 410 415

Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys Val Glu Glu Pro Lys
 420 425 430

Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser
 435 440 445

Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro Val Gln
450 455 460

Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn
465 470 475 480

Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly
485 490 495

Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala Pro Gln
500 505 510

Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser Thr Gly
515 520 525

Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro
530 535 540

Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn
545 550 555 560

Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp
565 570 575

Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu
580 585 590

Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe
595 600 605

Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val Ile
610 615 620

Lys Lys Asn Leu Ser Asp Phe Ile Ala
625 630

<210> 353

<211> 633

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 353

Met Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr Pro
1 5 10 15

Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His Glu
20 25 30

Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp Glu
35 40 45

Ser Gly Phe Val Met Ser Ser Gly Asp Ser Asn His Tyr Phe Phe Lys
50 55 60

Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu
65 70 75 80

Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser His Glu
85 90 95

Gln Asp Tyr Pro Gly Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys
100 105 110

Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg
115 120 125

Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro Ser
130 135 140

Gly Asp Gly His His Ala Asp Pro Ile Asp Glu His Lys Pro Val Gly
145 150 155 160

Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly
165 170 175

Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr
180 185 190

Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe
195 200 205

Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro Glu
210 215 220

Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr Pro
225 230 235 240

Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu Gly
245 250 255

Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly
260 265 270

Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser
275 280 285

Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala
290 295 300

Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg
305 310 315 320

Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg
325 330 335

Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys
340 345 350

Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr
355 360 365

Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala Tyr
370 375 380

Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu Glu Lys
385 390 395 400

Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn
405 410 415

Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys Val Glu Glu Pro Lys
420 425 430

Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser
435 440 445

Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro Val Gln
450 455 460

Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn
465 470 475 480

Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly
485 490 495

Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala Pro Gln
500 505 510

Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser Thr Gly
515 520 525

Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro
530 535 540

Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn
545 550 555 560

Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp
565 570 575

Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu
580 585 590

Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe
595 600 605

Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val Ile
610 615 620

Lys Lys Asn Leu Ser Asp Phe Ile Ala
625 630

<210> 354

<211> 633

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 354

Met Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr Pro
1 5 10 15

Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His Glu
20 25 30

Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp Glu
35 40 45

Ser Gly Phe Val Met Ser His Gly Asp His Asn His Tyr Phe Phe Lys
50 55 60

Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu
65 70 75 80

Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser His Glu
85 90 95

Gln Asp Tyr Pro Gly Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys
100 105 110

Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg
115 120 125

Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro Ser
130 135 140

Gly Asp His His His Ala Asp Pro Ile Asp Glu His Lys Pro Val Gly
145 150 155 160

Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly
165 170 175

Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr
180 185 190

Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe
195 200 205

Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro Glu
210 215 220

Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr Pro
 225 230 235 240

Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu Gly
 245 250 255

Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly
 260 265 270

Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser
 275 280 285

Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala
 290 295 300

Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg
 305 310 315 320

Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg
 325 330 335

Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys
 340 345 350

Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr
 355 360 365

Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala Tyr
 370 375 380

Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu Glu Lys
 385 390 395 400

Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn
 405 410 415

Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys Val Glu Glu Pro Lys
 420 425 430

Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser
 435 440 445

Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro Val Gln
450 455 460

Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn
465 470 475 480

Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly
485 490 495

Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala Pro Gln
500 505 510

Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser Thr Gly
515 520 525

Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro
530 535 540

Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn
545 550 555 560

Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp
565 570 575

Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu
580 585 590

Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe
595 600 605

Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val Ile
610 615 620

Lys Lys Asn Leu Ser Asp Phe Ile Ala
625 630

<210> 355

<211> 633

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 355

Met Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr Pro
1 5 10 15

Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His Glu
20 25 30

Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp Glu
35 40 45

Ser Gly Phe Val Met Ser His Gly Asp His Asn His Tyr Phe Phe Lys
50 55 60

Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu
65 70 75 80

Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser His Glu
85 90 95

Gln Asp Tyr Pro Gly Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys
100 105 110

Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg
115 120 125

Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro Ser
130 135 140

Gly Asp Gly His His Ala Asp Pro Ile Asp Glu His Lys Pro Val Gly
145 150 155 160

Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly
165 170 175

Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr
180 185 190

Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe
195 200 205

Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro Glu
210 215 220

Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr Pro
225 230 235 240

Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu Gly
245 250 255

Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly
260 265 270

Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser
275 280 285

Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala
290 295 300

Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg
305 310 315 320

Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg
325 330 335

Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys
340 345 350

Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr
355 360 365

Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala Tyr
370 375 380

Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu Glu Lys
385 390 395 400

Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn
405 410 415

Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys Val Glu Glu Pro Lys
420 425 430

Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser
435 440 445

Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro Val Gln

450

455

460

Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn
465 470 475 480

Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly
485 490 495

Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala Pro Gln
500 505 510

Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser Thr Gly
515 520 525

Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro
530 535 540

Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn
545 550 555 560

Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp
565 570 575

Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu
580 585 590

Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe
595 600 605

Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val Ile
610 615 620

Lys Lys Asn Leu Ser Asp Phe Ile Ala
625 630

<210> 356

<211> 569

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 356

Met Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu
1 5 10 15

Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser His Glu
20 25 30

Gln Asp Tyr Pro Gly Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys
35 40 45

Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg
50 55 60

Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro His
65 70 75 80

Gly Asp Gly His His Ala Asp Pro Ile Asp Glu His Lys Pro Val Gly
85 90 95

Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly
100 105 110

Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr
115 120 125

Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe
130 135 140

Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro Glu
145 150 155 160

Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr Pro
165 170 175

Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu Gly
180 185 190

Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly
195 200 205

Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser
210 215 220

Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala

225

230

235

240

Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg
 245 250 255

Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg
 260 265 270

Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys
 275 280 285

Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr
 290 295 300

Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala Tyr
 305 310 315 320

Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu Glu Lys
 325 330 335

Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn
 340 345 350

Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys Val Glu Glu Pro Lys
 355 360 365

Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser
 370 375 380

Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro Val Gln
 385 390 395 400

Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn
 405 410 415

Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly
 420 425 430

Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala Pro Gln
 435 440 445

Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser Thr Gly
 450 455 460

Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro
465 470 475 480

Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn
485 490 495

Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp
500 505 510

Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu
515 520 525

Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe
530 535 540

Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val Ile
545 550 555 560

Lys Lys Asn Leu Ser Asp Phe Ile Ala
565

<210> 357

<211> 633

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 357

Met Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr Pro
1 5 10 15

Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His Glu
20 25 30

Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp Glu
35 40 45

Ser Gly Phe Val Met Ser His Gly Asp Ser Asn His Tyr Phe Phe Lys
50 55 60

Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu

80

95

110

125

140

160

175

190

205

220

240

255

270

285

300

Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg
305 310 315 320

Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg
325 330 335

Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys
340 345 350

Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr
355 360 365

Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala Tyr
370 375 380

Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu Glu Lys
385 390 395 400

Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn
405 410 415

Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys Val Glu Glu Pro Lys
420 425 430

Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser
435 440 445

Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro Val Gln
450 455 460

Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn
465 470 475 480

Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly
485 490 495

Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala Pro Gln
500 505 510

Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser Thr Gly
515 520 525

Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro
530 535 540

Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn
545 550 555 560

Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp
565 570 575

Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu
580 585 590

Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe
595 600 605

Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val Ile
610 615 620

Lys Lys Asn Leu Ser Asp Phe Ile Ala
625 630

<210> 358

<211> 633

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 358

Met Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr Pro
1 5 10 15

Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His Glu
20 25 30

Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp Glu
35 40 45

Ser Gly Phe Val Met Ser His Gly Asp Ser Asn His Tyr Phe Phe Lys
50 55 60

Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu
65 70 75 80

Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser His Glu
85 90 95

Gln Asp Tyr Pro Gly Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys
100 105 110

Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg
115 120 125

Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro Ser
130 135 140

Gly Asp His His His Ala Asp Pro Ile Asp Glu His Lys Pro Val Gly
145 150 155 160

Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly
165 170 175

Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr
180 185 190

Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe
195 200 205

Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro Glu
210 215 220

Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr Pro
225 230 235 240

Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu Gly
245 250 255

Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly
260 265 270

Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser
275 280 285

Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala
290 295 300

Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg
 305 310 315 320

Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg
 325 330 335

Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys
 340 345 350

Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr
 355 360 365

Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala Tyr
 370 375 380

Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu Glu Lys
 385 390 395 400

Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn
 405 410 415

Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys Val Glu Glu Pro Lys
 420 425 430

Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser
 435 440 445

Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro Val Gln
 450 455 460

Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn
 465 470 475 480

Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly
 485 490 495

Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala Pro Gln
 500 505 510

Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser Thr Gly
 515 520 525

Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro
530 535 540

Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn
545 550 555 560

Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp
565 570 575

Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu
580 585 590

Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe
595 600 605

Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val Ile
610 615 620

Lys Lys Asn Leu Ser Asp Phe Ile Ala
625 630

<210> 359

<211> 633

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 359

Met Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr Pro
1 5 10 15

Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His Glu
20 25 30

Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp Glu
35 40 45

Ser Gly Phe Val Met Ser His Gly Asp Ser Asn His Tyr Phe Phe Lys
50 55 60

Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu
65 70 75 80

Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser His Glu
 85 90 95

Gln Asp Tyr Pro Gly Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys
 100 105 110

Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg
 115 120 125

Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro Ser
 130 135 140

Gly Asp His His His Ala Asp Pro Ile Asp Glu His Lys Pro Val Gly
 145 150 155 160

Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly
 165 170 175

Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr
 180 185 190

Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe
 195 200 205

Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro Glu
 210 215 220

Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr Pro
 225 230 235 240

Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu Gly
 245 250 255

Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly
 260 265 270

Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser
 275 280 285

Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala
 290 295 300

Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg
305 310 315 320

Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg
325 330 335

Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys
340 345 350

Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr
355 360 365

Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala Tyr
370 375 380

Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu Glu Lys
385 390 395 400

Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn
405 410 415

Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys Val Glu Glu Pro Lys
420 425 430

Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser
435 440 445

Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro Val Gln
450 455 460

Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn
465 470 475 480

Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly
485 490 495

Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala Pro Gln
500 505 510

Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser Thr Gly
515 520 525

Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro

530

535

540

Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn
 545 550 555 560

Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp
 565 570 575

Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu
 580 585 590

Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe
 595 600 605

Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val Ile
 610 615 620

Lys Lys Asn Leu Ser Asp Phe Ile Ala
 625 630

<210> 360

<211> 633

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 360

Met Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr Pro
 1 5 10 15

Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His Glu
 20 25 30

Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp Glu
 35 40 45

Ser Gly Phe Val Met Ser His Gly Asp His Asn Ser Tyr Phe Phe Lys
 50 55 60

Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu
 65 70 75 80

Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser His Glu
85 90 95

Gln Asp Tyr Pro Gly Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys
100 105 110

Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg
115 120 125

Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro Ser
130 135 140

Gly Asp His His His Ala Asp Pro Ile Asp Glu His Lys Pro Val Gly
145 150 155 160

Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly
165 170 175

Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr
180 185 190

Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe
195 200 205

Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro Glu
210 215 220

Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr Pro
225 230 235 240

Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu Gly
245 250 255

Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly
260 265 270

Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser
275 280 285

Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala
290 295 300

Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg

305	310	315	320
Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg	325	330	335
Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys	340	345	350
Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr	355	360	365
Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala Tyr	370	375	380
Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu Glu Lys	385	390	395
Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn	405	410	415
Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys Val Glu Glu Pro Lys	420	425	430
Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser	435	440	445
Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro Val Gln	450	455	460
Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn	465	470	475
Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly	485	490	495
Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala Pro Gln	500	505	510
Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser Thr Gly	515	520	525
Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro	530	535	540

Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn
545 550 555 560

Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp
565 570 575

Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu
580 585 590

Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe
595 600 605

Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val Ile
610 615 620

Lys Lys Asn Leu Ser Asp Phe Ile Ala
625 630

<210> 361

<211> 633

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 361

Met Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr Pro
1 5 10 15

Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His Glu
20 25 30

Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp Glu
35 40 45

Ser Gly Phe Val Met Ser His Gly Asp Ser Asn His Tyr Phe Phe Lys
50 55 60

Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu
65 70 75 80

Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser His Glu

85

90

95

Gln Asp Tyr Pro Gly Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys
 100 105 110

Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg
 115 120 125

Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro His
 130 135 140

Gly Asp His His His Ala Asp Pro Ile Asp Glu His Lys Pro Val Gly
 145 150 155 160

Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly
 165 170 175

Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr
 180 185 190

Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe
 195 200 205

Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro Glu
 210 215 220

Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr Pro
 225 230 235 240

Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu Gly
 245 250 255

Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly
 260 265 270

Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser
 275 280 285

Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala
 290 295 300

Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg
 305 310 315 320

Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg
325 330 335

Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys
340 345 350

Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr
355 360 365

Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala Tyr
370 375 380

Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu Glu Lys
385 390 395 400

Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn
405 410 415

Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys Val Glu Glu Pro Lys
420 425 430

Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser
435 440 445

Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro Val Gln
450 455 460

Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn
465 470 475 480

Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly
485 490 495

Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala Pro Gln
500 505 510

Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser Thr Gly
515 520 525

Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro
530 535 540

Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn
545 550 555 560

Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp
565 570 575

Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu
580 585 590

Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe
595 600 605

Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val Ile
610 615 620

Lys Lys Asn Leu Ser Asp Phe Ile Ala
625 630

<210> 362

<211> 633

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 362

Met Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr Pro
1 5 10 15

Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His Glu
20 25 30

Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp Glu
35 40 45

Ser Gly Phe Val Met Ser His Gly Asp His Asn Ser Tyr Phe Phe Lys
50 55 60

Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu
65 70 75 80

Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser His Glu
85 90 95

Gln Asp Tyr Pro Gly Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys
 100 105 110

Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg
 115 120 125

Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro His
 130 135 140

Gly Asp His His His Ala Asp Pro Ile Asp Glu His Lys Pro Val Gly
 145 150 155 160

Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly
 165 170 175

Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr
 180 185 190

Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe
 195 200 205

Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro Glu
 210 215 220

Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr Pro
 225 230 235 240

Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu Gly
 245 250 255

Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly
 260 265 270

Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser
 275 280 285

Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala
 290 295 300

Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg
 305 310 315 320

Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg
325 330 335

Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys
340 345 350

Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr
355 360 365

Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala Tyr
370 375 380

Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu Glu Lys
385 390 395 400

Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn
405 410 415

Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys Val Glu Glu Pro Lys
420 425 430

Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser
435 440 445

Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro Val Gln
450 455 460

Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn
465 470 475 480

Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly
485 490 495

Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala Pro Gln
500 505 510

Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser Thr Gly
515 520 525

Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro
530 535 540

Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn
545 550 555 560

Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp
565 570 575

Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu
580 585 590

Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe
595 600 605

Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val Ile
610 615 620

Lys Lys Asn Leu Ser Asp Phe Ile Ala
625 630

<210> 363

<211> 633

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 363

Met Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr Pro
1 5 10 15

Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His Glu
20 25 30

Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp Glu
35 40 45

Ser Gly Phe Val Met Ser His Gly Asp Ser Asn His Tyr Phe Phe Lys
50 55 60

Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu
65 70 75 80

Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser His Glu
85 90 95

Gln Asp Tyr Pro Gly Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys
100 105 110

Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg
115 120 125

Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro His
130 135 140

Gly Asp Gly His His Ala Asp Pro Ile Asp Glu His Lys Pro Val Gly
145 150 155 160

Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly
165 170 175

Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr
180 185 190

Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe
195 200 205

Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro Glu
210 215 220

Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr Pro
225 230 235 240

Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu Gly
245 250 255

Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly
260 265 270

Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser
275 280 285

Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala
290 295 300

Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg
305 310 315 320

Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg
325 330 335

Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys
340 345 350

Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr
355 360 365

Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala Tyr
370 375 380

Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu Glu Lys
385 390 395 400

Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn
405 410 415

Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys Val Glu Glu Pro Lys
420 425 430

Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser
435 440 445

Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro Val Gln
450 455 460

Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn
465 470 475 480

Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly
485 490 495

Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala Pro Gln
500 505 510

Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser Thr Gly
515 520 525

Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro
530 535 540

Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn

545

550

555

560

Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp
565 570 575

Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu
580 585 590

Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe
595 600 605

Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val Ile
610 615 620

Lys Lys Asn Leu Ser Asp Phe Ile Ala
625 630

<210> 364

<211> 633

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 364

Met Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr Pro
1 5 10 15

Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His Glu
20 25 30

Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp Glu
35 40 45

Ser Gly Phe Val Met Ser His Gly Asp His Asn Ser Tyr Phe Phe Lys
50 55 60

Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu
65 70 75 80

Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser His Glu
85 90 95

Gln Asp Tyr Pro Gly Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys
100 105 110

Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg
115 120 125

Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro His
130 135 140

Gly Asp Gly His His Ala Asp Pro Ile Asp Glu His Lys Pro Val Gly
145 150 155 160

Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly
165 170 175

Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr
180 185 190

Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe
195 200 205

Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro Glu
210 215 220

Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr Pro
225 230 235 240

Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu Gly
245 250 255

Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly
260 265 270

Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser
275 280 285

Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala
290 295 300

Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg
305 310 315 320

Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg

325

330

335

Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys
 340 345 350

Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr
 355 360 365

Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala Tyr
 370 375 380

Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu Glu Lys
 385 390 395 400

Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn
 405 410 415

Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys Val Glu Glu Pro Lys
 420 425 430

Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser
 435 440 445

Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro Val Gln
 450 455 460

Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn
 465 470 475 480

Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly
 485 490 495

Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala Pro Gln
 500 505 510

Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser Thr Gly
 515 520 525

Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro
 530 535 540

Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn
 545 550 555 560

Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp
565 570 575

Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu
580 585 590

Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe
595 600 605

Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val Ile
610 615 620

Lys Lys Asn Leu Ser Asp Phe Ile Ala
625 630

<210> 365
<211> 633
<212> PRT
<213> Artificial Sequence

<220>
<223> Unknown Organism

<400> 365

Met Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr Pro
1 5 10 15

Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His Glu
20 25 30

Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp Glu
35 40 45

Ser Gly Phe Val Met Ser His Gly Asp His Asn Ser Tyr Phe Phe Lys
50 55 60

Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu
65 70 75 80

Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser His Glu
85 90 95

Gln Asp Tyr Pro Gly Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys

100

105

110

Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg
 115 120 125

Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro Ser
 130 135 140

Gly Asp Gly His His Ala Asp Pro Ile Asp Glu His Lys Pro Val Gly
 145 150 155 160

Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly
 165 170 175

Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr
 180 185 190

Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe
 195 200 205

Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro Glu
 210 215 220

Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr Pro
 225 230 235 240

Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu Gly
 245 250 255

Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly
 260 265 270

Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser
 275 280 285

Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala
 290 295 300

Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg
 305 310 315 320

Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg
 325 330 335

Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys
340 345 350

Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr
355 360 365

Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala Tyr
370 375 380

Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu Glu Lys
385 390 395 400

Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn
405 410 415

Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys Val Glu Glu Pro Lys
420 425 430

Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser
435 440 445

Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro Val Gln
450 455 460

Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn
465 470 475 480

Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly
485 490 495

Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala Pro Gln
500 505 510

Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser Thr Gly
515 520 525

Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro
530 535 540

Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn
545 550 555 560

Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp
565 570 575

Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu
580 585 590

Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe
595 600 605

Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val Ile
610 615 620

Lys Lys Asn Leu Ser Asp Phe Ile Ala
625 630

<210> 366
<211> 627
<212> PRT
<213> Artificial Sequence

<220>
<223> Unknown Organism

<400> 366

Met Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr Pro
1 5 10 15

Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His Glu
20 25 30

Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp Glu
35 40 45

Ser Gly Phe Val Met Ser Tyr Phe Phe Lys Lys Asp Leu Thr Glu Glu
50 55 60

Gln Ile Lys Ala Ala Gln Lys His Leu Glu Glu Val Lys Thr Ser His
65 70 75 80

Asn Gly Leu Asp Ser Leu Ser Ser His Glu Gln Asp Tyr Pro Gly Asn
85 90 95

Ala Lys Glu Met Lys Asp Leu Asp Lys Lys Ile Glu Glu Lys Ile Ala
100 105 110

Gly Ile Met Lys Gln Tyr Gly Val Lys Arg Glu Ser Ile Val Val Asn
115 120 125

Lys Glu Lys Asn Ala Ile Ile Tyr Pro His Gly Asp His His His Ala
130 135 140

Asp Pro Ile Asp Glu His Lys Pro Val Gly Ile Gly His Ser His Ser
145 150 155 160

Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly Val Ala Lys Lys Glu Gly
165 170 175

Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr Asn Val Val Asn Leu Leu
180 185 190

Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe Thr Leu Ala Asn Gly Gln
195 200 205

Lys Arg Val Ser Phe Ser Phe Pro Pro Glu Leu Glu Lys Lys Leu Gly
210 215 220

Ile Asn Met Leu Val Lys Leu Ile Thr Pro Asp Gly Lys Val Leu Glu
225 230 235 240

Lys Val Ser Gly Lys Val Phe Gly Glu Gly Val Gly Asn Ile Ala Asn
245 250 255

Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly Gln Thr Phe Lys Tyr Thr
260 265 270

Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser Tyr Asp Gly Thr Phe Thr
275 280 285

Val Pro Thr Ser Leu Ala Tyr Lys Met Ala Ser Gln Thr Ile Phe Tyr
290 295 300

Pro Phe His Ala Gly Asp Thr Tyr Leu Arg Val Asn Pro Gln Phe Ala
305 310 315 320

Val Pro Lys Gly Thr Asp Ala Leu Val Arg Val Phe Asp Glu Phe His
325 330 335

Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys Val Gly Glu Ile Lys Leu
340 345 350

Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr Arg Thr Ala Gly Asn Lys
355 360 365

Ile Pro Val Thr Phe Met Ala Asn Ala Tyr Leu Asp Asn Gln Ser Thr
370 375 380

Tyr Ile Val Glu Val Pro Ile Leu Glu Lys Glu Asn Gln Thr Asp Lys
385 390 395 400

Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn Lys Ala Gln Glu Asn Ser
405 410 415

Lys Leu Asp Glu Lys Val Glu Glu Pro Lys Thr Ser Glu Lys Val Glu
420 425 430

Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser Thr Ser Asn Ser Thr Leu
435 440 445

Glu Glu Val Pro Thr Val Asp Pro Val Gln Glu Lys Val Ala Lys Phe
450 455 460

Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn Val Leu Phe Asn Met Asp
465 470 475 480

Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly Glu Val Ile Lys Lys Asn
485 490 495

Met Ala Asp Phe Thr Gly Glu Ala Pro Gln Gly Asn Gly Glu Asn Lys
500 505 510

Pro Ser Glu Asn Gly Lys Val Ser Thr Gly Thr Val Glu Asn Gln Pro
515 520 525

Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro Glu Ala Pro Asn Glu Lys
530 535 540

Pro Val Lys Pro Glu Asn Ser Thr Asp Asn Gly Met Leu Asn Pro Glu
545 550 555 560

Gly Asn Val Gly Ser Asp Pro Met Leu Asp Pro Ala Leu Glu Glu Ala
565 570 575

Pro Ala Val Asp Pro Val Gln Glu Lys Leu Glu Lys Phe Thr Ala Ser
580 585 590

Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe Asn Met Asp Gly Thr Ile
595 600 605

Glu Leu Arg Leu Pro Ser Gly Glu Val Ile Lys Lys Asn Leu Ser Asp
610 615 620

Phe Ile Ala
625

<210> 367
<211> 627
<212> PRT
<213> Artificial Sequence

<220>
<223> Unknown Organism

<400> 367

Met Gln Ile Cys Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr Pro
1 5 10 15

Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His Glu
20 25 30

Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp Glu
35 40 45

Ser Gly Phe Val Met Ser His Gly Asp His Asn His Tyr Phe Phe Lys
50 55 60

Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu
65 70 75 80

Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser His Glu
85 90 95

Gln Asp Tyr Pro Gly Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys
100 105 110

Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg
115 120 125

Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro Ala
130 135 140

Asp Pro Ile Asp Glu His Lys Pro Val Gly Ile Gly His Ser His Ser
145 150 155 160

Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly Val Ala Lys Lys Glu Gly
165 170 175

Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr Asn Val Val Asn Leu Leu
180 185 190

Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe Thr Leu Ala Asn Gly Gln
195 200 205

Lys Arg Val Ser Phe Ser Phe Pro Pro Glu Leu Glu Lys Lys Leu Gly
210 215 220

Ile Asn Met Leu Val Lys Leu Ile Thr Pro Asp Gly Lys Val Leu Glu
225 230 235 240

Lys Val Ser Gly Lys Val Phe Gly Glu Gly Val Gly Asn Ile Ala Asn
245 250 255

Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly Gln Thr Phe Lys Tyr Thr
260 265 270

Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser Tyr Asp Gly Thr Phe Thr
275 280 285

Val Pro Thr Ser Leu Ala Tyr Lys Met Ala Ser Gln Thr Ile Phe Tyr
290 295 300

Pro Phe His Ala Gly Asp Thr Tyr Leu Arg Val Asn Pro Gln Phe Ala
305 310 315 320

Val Pro Lys Gly Thr Asp Ala Leu Val Arg Val Phe Asp Glu Phe His
325 330 335

Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys Val Gly Glu Ile Lys Leu
340 345 350

Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr Arg Thr Ala Gly Asn Lys
355 360 365

Ile Pro Val Thr Phe Met Ala Asn Ala Tyr Leu Asp Asn Gln Ser Thr
370 375 380

Tyr Ile Val Glu Val Pro Ile Leu Glu Lys Glu Asn Gln Thr Asp Lys
385 390 395 400

Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn Lys Ala Gln Glu Asn Ser
405 410 415

Lys Leu Asp Glu Lys Val Glu Glu Pro Lys Thr Ser Glu Lys Val Glu
420 425 430

Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser Thr Ser Asn Ser Thr Leu
435 440 445

Glu Glu Val Pro Thr Val Asp Pro Val Gln Glu Lys Val Ala Lys Phe
450 455 460

Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn Val Leu Phe Asn Met Asp
465 470 475 480

Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly Glu Val Ile Lys Lys Asn
485 490 495

Met Ala Asp Phe Thr Gly Glu Ala Pro Gln Gly Asn Gly Glu Asn Lys
500 505 510

Pro Ser Glu Asn Gly Lys Val Ser Thr Gly Thr Val Glu Asn Gln Pro
515 520 525

Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro Glu Ala Pro Asn Glu Lys
530 535 540

Pro Val Lys Pro Glu Asn Ser Thr Asp Asn Gly Met Leu Asn Pro Glu
545 550 555 560

Gly Asn Val Gly Ser Asp Pro Met Leu Asp Pro Ala Leu Glu Glu Ala

565

570

575

Pro Ala Val Asp Pro Val Gln Glu Lys Leu Glu Lys Phe Thr Ala Ser
 580 585 590

Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe Asn Met Asp Gly Thr Ile
 595 600 605

Glu Leu Arg Leu Pro Ser Gly Glu Val Ile Lys Lys Asn Leu Ser Asp
 610 615 620

Phe Ile Ala
 625

<210> 368

<211> 621

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 368

Met Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr Pro
 1 5 10 15

Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His Glu
 20 25 30

Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp Glu
 35 40 45

Ser Gly Phe Val Met Ser Tyr Phe Phe Lys Lys Asp Leu Thr Glu Glu
 50 55 60

Gln Ile Lys Ala Ala Gln Lys His Leu Glu Glu Val Lys Thr Ser His
 65 70 75 80

Asn Gly Leu Asp Ser Leu Ser Ser His Glu Gln Asp Tyr Pro Gly Asn
 85 90 95

Ala Lys Glu Met Lys Asp Leu Asp Lys Lys Ile Glu Glu Lys Ile Ala
 100 105 110

Gly Ile Met Lys Gln Tyr Gly Val Lys Arg Glu Ser Ile Val Val Asn
115 120 125

Lys Glu Lys Asn Ala Ile Ile Tyr Pro Ala Asp Pro Ile Asp Glu His
130 135 140

Lys Pro Val Gly Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys
145 150 155 160

Pro Glu Glu Gly Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly
165 170 175

Glu Glu Leu Thr Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn
180 185 190

Asn Gln Asn Phe Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser
195 200 205

Phe Pro Pro Glu Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys
210 215 220

Leu Ile Thr Pro Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val
225 230 235 240

Phe Gly Glu Gly Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro
245 250 255

Tyr Leu Pro Gly Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr
260 265 270

Pro Glu Val Ser Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala
275 280 285

Tyr Lys Met Ala Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp
290 295 300

Thr Tyr Leu Arg Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp
305 310 315 320

Ala Leu Val Arg Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu
325 330 335

Asn Asn Tyr Lys Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn

340

345

350

Gln Gly Thr Thr Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met
 355 360 365

Ala Asn Ala Tyr Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro
 370 375 380

Ile Leu Glu Lys Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln
 385 390 395 400

Phe Lys Arg Asn Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys Val
 405 410 415

Glu Glu Pro Lys Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu
 420 425 430

Thr Gly Asn Ser Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val
 435 440 445

Asp Pro Val Gln Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met
 450 455 460

Lys Leu Glu Asn Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr
 465 470 475 480

Leu Pro Ser Gly Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly
 485 490 495

Glu Ala Pro Gln Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys
 500 505 510

Val Ser Thr Gly Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala
 515 520 525

Asp Ser Leu Pro Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn
 530 535 540

Ser Thr Asp Asn Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp
 545 550 555 560

Pro Met Leu Asp Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val
 565 570 575

Gln Glu Lys Leu Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp
580 585 590

Ser Val Ile Phe Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser
595 600 605

Gly Glu Val Ile Lys Lys Asn Leu Ser Asp Phe Ile Ala
610 615 620

<210> 369
<211> 906
<212> PRT
<213> Artificial Sequence

<220>
<223> Unknown Organism

<400> 369

Met Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr Pro
1 5 10 15

Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His Glu
20 25 30

Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp Glu
35 40 45

Ser Gly Phe Val Met Ser His Gly Asp Ser Asn His Tyr Phe Phe Lys
50 55 60

Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu
65 70 75 80

Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser His Glu
85 90 95

Gln Asp Tyr Pro Gly Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys
100 105 110

Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg
115 120 125

Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro Ser

130

135

140

Gly Asp His His His Ala Asp Pro Ile Asp Glu His Lys Pro Val Gly
145 150 155 160

Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly
165 170 175

Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr
180 185 190

Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe
195 200 205

Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro Glu
210 215 220

Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr Pro
225 230 235 240

Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu Gly
245 250 255

Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly
260 265 270

Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser
275 280 285

Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala
290 295 300

Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg
305 310 315 320

Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg
325 330 335

Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys
340 345 350

Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr
355 360 365

Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala Tyr
370 375 380

Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu Glu Lys
385 390 395 400

Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn
405 410 415

Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys Val Glu Glu Pro Lys
420 425 430

Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser
435 440 445

Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro Val Gln
450 455 460

Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn
465 470 475 480

Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly
485 490 495

Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala Pro Gln
500 505 510

Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser Thr Gly
515 520 525

Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro
530 535 540

Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn
545 550 555 560

Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp
565 570 575

Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu
580 585 590

Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe
595 600 605

Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val Ile
610 615 620

Lys Lys Asn Leu Ser Asp Phe Ile Ala Gly Pro Gln Ile Thr Tyr Thr
625 630 635 640

Asp Asp Glu Ile Gln Val Ala Lys Leu Ala Gly Lys Tyr Thr Thr Glu
645 650 655

Asp Gly Tyr Ile Phe Asp Thr Ser Trp Ile Lys Lys Asp Ser Leu Ser
660 665 670

Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr Ala Lys Glu Lys Gly Leu
675 680 685

Thr Pro Pro Ser Thr Asp His Gln Asp Ser Gly Asn Thr Glu Ala Lys
690 695 700

Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys Ala Ala Lys Lys Val Pro
705 710 715 720

Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr Thr Val Glu Val Lys Asn
725 730 735

Gly Ser Leu Ile Ile Pro His Tyr Asp His Tyr His Asn Ile Lys Phe
740 745 750

Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala Pro Lys Gly Tyr Ser Leu
755 760 765

Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr Val Glu Pro Arg Asn Ala
770 775 780

Ser Asp His Val Arg Lys Asn Lys Ala Asp Gln Asp Ser Lys Pro Asp
785 790 795 800

Glu Asp Lys Glu His Asp Glu Val Ser Glu Pro Thr His Pro Glu Ser
805 810 815

Asp Glu Lys Glu Asn His Ala Gly Leu Asn Pro Ser Ala Asp Asn Leu
820 825 830

Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr Glu Glu Glu Ala Glu Asp
835 840 845

Thr Thr Asp Glu Ala Glu Ile Pro Gly Thr Pro Ser Ile Arg Gln Asn
850 855 860

Ala Met Glu Thr Leu Thr Gly Leu Lys Ser Ser Leu Leu Leu Gly Thr
865 870 875 880

Lys Asp Asn Asn Thr Ile Ser Ala Glu Val Asp Ser Leu Leu Ala Leu
885 890 895

Leu Lys Glu Ser Gln Pro Ala Pro Ile Gln
900 905

<210> 370
<211> 906
<212> PRT
<213> Artificial Sequence

<220>
<223> Unknown Organism

<400> 370

Met Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
1 5 10 15

Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Thr Ser Trp Ile
20 25 30

Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr
35 40 45

Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser
50 55 60

Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys
65 70 75 80

Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr
85 90 95

Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro His Tyr Asp His
100 105 110

Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala
115 120 125

Pro Lys Gly Tyr Ser Leu Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr
130 135 140

Val Glu Pro Arg Asn Ala Ser Asp His Val Arg Lys Asn Lys Ala Asp
145 150 155 160

Gln Asp Ser Lys Pro Asp Glu Asp Lys Glu His Asp Glu Val Ser Glu
165 170 175

Pro Thr His Pro Glu Ser Asp Glu Lys Glu Asn His Ala Gly Leu Asn
180 185 190

Pro Ser Ala Asp Asn Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr
195 200 205

Glu Glu Glu Ala Glu Asp Thr Thr Asp Glu Ala Glu Ile Pro Gly Thr
210 215 220

Pro Ser Ile Arg Gln Asn Ala Met Glu Thr Leu Thr Gly Leu Lys Ser
225 230 235 240

Ser Leu Leu Leu Gly Thr Lys Asp Asn Asn Thr Ile Ser Ala Glu Val
245 250 255

Asp Ser Leu Leu Ala Leu Leu Lys Glu Ser Gln Pro Ala Pro Ile Gln
260 265 270

Gly Pro Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr
275 280 285

Pro Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His
290 295 300

Glu Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp
305 310 315 320

Glu Ser Gly Phe Val Met Ser His Gly Asp Ser Asn His Tyr Phe Phe
325 330 335

Lys Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu
340 345 350

Glu Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser His
355 360 365

Glu Gln Asp Tyr Pro Gly Asn Ala Lys Glu Met Lys Asp Leu Asp Lys
370 375 380

Lys Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys
385 390 395 400

Arg Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro
405 410 415

Ser Gly Asp His His His Ala Asp Pro Ile Asp Glu His Lys Pro Val
420 425 430

Gly Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu
435 440 445

Gly Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu
450 455 460

Thr Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn
465 470 475 480

Phe Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro
485 490 495

Glu Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr
500 505 510

Pro Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu
515 520 525

Gly Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro
530 535 540

Gly Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val

545

550

555

560

Ser Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met
565 570 575

Ala Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu
580 585 590

Arg Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val
595 600 605

Arg Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr
610 615 620

Lys Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr
625 630 635 640

Thr Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala
645 650 655

Tyr Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu Glu
660 665 670

Lys Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg
675 680 685

Asn Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys Val Glu Glu Pro
690 695 700

Lys Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn
705 710 715 720

Ser Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro Val
725 730 735

Gln Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu
740 745 750

Asn Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser
755 760 765

Gly Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala Pro
770 775 780

Gln Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser Thr
785 790 795 800

Gly Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu
805 810 815

Pro Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp
820 825 830

Asn Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu
835 840 845

Asp Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys
850 855 860

Leu Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile
865 870 875 880

Phe Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val
885 890 895

Ile Lys Lys Asn Leu Ser Asp Phe Ile Ala
900 905

<210> 371
<211> 906
<212> PRT
<213> Artificial Sequence

<220>
<223> Unknown Organism

<400> 371

Met Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr Pro
1 5 10 15

Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His Glu
20 25 30

Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp Glu
35 40 45

Ser Gly Phe Val Met Ser Ser Gly Asp Ser Asn His Tyr Phe Phe Lys

50

55

60

Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu
65 70 75 80

Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser His Glu
85 90 95

Gln Asp Tyr Pro Gly Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys
100 105 110

Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg
115 120 125

Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro Ser
130 135 140

Gly Asp Gly His His Ala Asp Pro Ile Asp Glu His Lys Pro Val Gly
145 150 155 160

Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly
165 170 175

Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr
180 185 190

Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe
195 200 205

Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro Glu
210 215 220

Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr Pro
225 230 235 240

Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu Gly
245 250 255

Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly
260 265 270

Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser
275 280 285

Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala
290 295 300

Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg
305 310 315 320

Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg
325 330 335

Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys
340 345 350

Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr
355 360 365

Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala Tyr
370 375 380

Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu Glu Lys
385 390 395 400

Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn
405 410 415

Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys Val Glu Glu Pro Lys
420 425 430

Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser
435 440 445

Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro Val Gln
450 455 460

Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn
465 470 475 480

Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly
485 490 495

Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala Pro Gln
500 505 510

Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser Thr Gly
515 520 525

Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro
530 535 540

Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn
545 550 555 560

Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp
565 570 575

Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu
580 585 590

Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe
595 600 605

Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val Ile
610 615 620

Lys Lys Asn Leu Ser Asp Phe Ile Ala Gly Pro Gln Ile Thr Tyr Thr
625 630 635 640

Asp Asp Glu Ile Gln Val Ala Lys Leu Ala Gly Lys Tyr Thr Thr Glu
645 650 655

Asp Gly Tyr Ile Phe Asp Thr Ser Trp Ile Lys Lys Asp Ser Leu Ser
660 665 670

Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr Ala Lys Glu Lys Gly Leu
675 680 685

Thr Pro Pro Ser Thr Asp His Gln Asp Ser Gly Asn Thr Glu Ala Lys
690 695 700

Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys Ala Ala Lys Lys Val Pro
705 710 715 720

Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr Thr Val Glu Val Lys Asn
725 730 735

Gly Ser Leu Ile Ile Pro His Tyr Asp His Tyr His Asn Ile Lys Phe
740 745 750

Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala Pro Lys Gly Tyr Ser Leu
755 760 765

Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr Val Glu Pro Arg Asn Ala
770 775 780

Ser Asp His Val Arg Lys Asn Lys Ala Asp Gln Asp Ser Lys Pro Asp
785 790 795 800

Glu Asp Lys Glu His Asp Glu Val Ser Glu Pro Thr His Pro Glu Ser
805 810 815

Asp Glu Lys Glu Asn His Ala Gly Leu Asn Pro Ser Ala Asp Asn Leu
820 825 830

Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr Glu Glu Glu Ala Glu Asp
835 840 845

Thr Thr Asp Glu Ala Glu Ile Pro Gly Thr Pro Ser Ile Arg Gln Asn
850 855 860

Ala Met Glu Thr Leu Thr Gly Leu Lys Ser Ser Leu Leu Leu Gly Thr
865 870 875 880

Lys Asp Asn Asn Thr Ile Ser Ala Glu Val Asp Ser Leu Leu Ala Leu
885 890 895

Leu Lys Glu Ser Gln Pro Ala Pro Ile Gln
900 905

<210> 372

<211> 906

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 372

Met Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
1 5 10 15

Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Thr Ser Trp Ile
20 25 30

Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr
35 40 45

Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser
50 55 60

Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys
65 70 75 80

Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr
85 90 95

Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro His Tyr Asp His
100 105 110

Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala
115 120 125

Pro Lys Gly Tyr Ser Leu Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr
130 135 140

Val Glu Pro Arg Asn Ala Ser Asp His Val Arg Lys Asn Lys Ala Asp
145 150 155 160

Gln Asp Ser Lys Pro Asp Glu Asp Lys Glu His Asp Glu Val Ser Glu
165 170 175

Pro Thr His Pro Glu Ser Asp Glu Lys Glu Asn His Ala Gly Leu Asn
180 185 190

Pro Ser Ala Asp Asn Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr
195 200 205

Glu Glu Glu Ala Glu Asp Thr Thr Asp Glu Ala Glu Ile Pro Gly Thr
210 215 220

Pro Ser Ile Arg Gln Asn Ala Met Glu Thr Leu Thr Gly Leu Lys Ser
225 230 235 240

Ser Leu Leu Leu Gly Thr Lys Asp Asn Asn Thr Ile Ser Ala Glu Val
245 250 255

Asp Ser Leu Leu Ala Leu Leu Lys Glu Ser Gln Pro Ala Pro Ile Gln
260 265 270

Gly Pro Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr
275 280 285

Pro Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His
290 295 300

Glu Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp
305 310 315 320

Glu Ser Gly Phe Val Met Ser Ser Gly Asp Ser Asn His Tyr Phe Phe
325 330 335

Lys Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu
340 345 350

Glu Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser His
355 360 365

Glu Gln Asp Tyr Pro Gly Asn Ala Lys Glu Met Lys Asp Leu Asp Lys
370 375 380

Lys Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys
385 390 395 400

Arg Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro
405 410 415

Ser Gly Asp Gly His His Ala Asp Pro Ile Asp Glu His Lys Pro Val
420 425 430

Gly Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu
435 440 445

Gly Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu
450 455 460

Thr Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn

465		470		475		480
Phe Thr Leu Ala	Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro	485		490		495
Glu Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr		500		505		510
Pro Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu		515		520		525
Gly Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro		530		535		540
Gly Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val		545		550		555
Ser Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met		565		570		575
Ala Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu		580		585		590
Arg Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val		595		600		605
Arg Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr		610		615		620
Lys Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr		625		630		635
Thr Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala		645		650		655
Tyr Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu Glu		660		665		670
Lys Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg		675		680		685
Asn Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys Val Glu Glu Pro		690		695		700

Lys Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn
705 710 715 720

Ser Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro Val
725 730 735

Gln Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu
740 745 750

Asn Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser
755 760 765

Gly Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala Pro
770 775 780

Gln Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser Thr
785 790 795 800

Gly Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu
805 810 815

Pro Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp
820 825 830

Asn Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu
835 840 845

Asp Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys
850 855 860

Leu Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile
865 870 875 880

Phe Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val
885 890 895

Ile Lys Lys Asn Leu Ser Asp Phe Ile Ala
900 905

<210> 373

<211> 906

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 373

Met Gln Ile Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr Pro
1 5 10 15

Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His Glu
20 25 30

Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp Glu
35 40 45

Ser Gly Phe Val Met Ser His Gly Asp Ser Asn His Tyr Phe Phe Lys
50 55 60

Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu
65 70 75 80

Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser His Glu
85 90 95

Gln Asp Tyr Pro Gly Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys
100 105 110

Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg
115 120 125

Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro Ser
130 135 140

Gly Asp His His His Ala Asp Pro Ile Asp Glu His Lys Pro Val Gly
145 150 155 160

Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly
165 170 175

Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr
180 185 190

Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe
195 200 205

Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro Glu
210 215 220

Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr Pro
225 230 235 240

Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu Gly
245 250 255

Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly
260 265 270

Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser
275 280 285

Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala
290 295 300

Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg
305 310 315 320

Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg
325 330 335

Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys
340 345 350

Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr
355 360 365

Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala Tyr
370 375 380

Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu Glu Lys
385 390 395 400

Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn
405 410 415

Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys Val Glu Glu Pro Lys
420 425 430

Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser
435 440 445

Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro Val Gln
450 455 460

Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn
465 470 475 480

Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly
485 490 495

Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala Pro Gln
500 505 510

Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser Thr Gly
515 520 525

Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro
530 535 540

Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn
545 550 555 560

Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp
565 570 575

Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu
580 585 590

Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe
595 600 605

Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val Ile
610 615 620

Lys Lys Asn Leu Ser Asp Phe Ile Ala Gly Pro Gln Ile Thr Tyr Thr
625 630 635 640

Asp Asp Glu Ile Gln Val Ala Lys Leu Ala Gly Lys Tyr Thr Thr Glu
645 650 655

Asp Gly Tyr Ile Phe Asp Thr Ser Trp Ile Lys Lys Asp Ser Leu Ser
660 665 670

Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr Ala Lys Glu Lys Gly Leu
675 680 685

Thr Pro Pro Ser Thr Asp His Gln Asp Ser Gly Asn Thr Glu Ala Lys
690 695 700

Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys Ala Ala Lys Lys Val Pro
705 710 715 720

Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr Thr Val Glu Val Lys Asn
725 730 735

Gly Ser Leu Ile Ile Pro Ser Tyr Asp His Tyr His Asn Ile Lys Phe
740 745 750

Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala Pro Lys Gly Tyr Ser Leu
755 760 765

Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr Val Glu Pro Arg Asn Ala
770 775 780

Ser Asp His Val Arg Lys Asn Lys Ala Asp Gln Asp Ser Lys Pro Asp
785 790 795 800

Glu Asp Lys Glu His Asp Glu Val Ser Glu Pro Thr His Pro Glu Ser
805 810 815

Asp Glu Lys Glu Asn His Ala Gly Leu Asn Pro Ser Ala Asp Asn Leu
820 825 830

Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr Glu Glu Glu Ala Glu Asp
835 840 845

Thr Thr Asp Glu Ala Glu Ile Pro Gly Thr Pro Ser Ile Arg Gln Asn
850 855 860

Ala Met Glu Thr Leu Thr Gly Leu Lys Ser Ser Leu Leu Leu Gly Thr
865 870 875 880

Lys Asp Asn Asn Thr Ile Ser Ala Glu Val Asp Ser Leu Leu Ala Leu

885

890

895

Leu Lys Glu Ser Gln Pro Ala Pro Ile Gln
 900 905

<210> 374

<211> 259

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 374

Met Leu Ala Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Thr
 1 5 10 15

Ser Trp Ile Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala
 20 25 30

Gln Ala Tyr Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His
 35 40 45

Gln Asp Ser Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn
 50 55 60

Arg Val Lys Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn
 65 70 75 80

Leu Gln Tyr Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro His
 85 90 95

Tyr Asp His Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu
 100 105 110

Tyr Glu Ala Pro Lys Gly Tyr Ser Leu Glu Asp Leu Leu Ala Thr Val
 115 120 125

Lys Tyr Tyr Val Glu Pro Arg Asn Ala Ser Asp His Val Arg Lys Asn
 130 135 140

Lys Ala Asp Gln Asp Ser Lys Pro Asp Glu Asp Lys Glu His Asp Glu
 145 150 155 160

Val Ser Glu Pro Thr His Pro Glu Ser Asp Glu Lys Glu Asn His Ala
165 170 175

Gly Leu Asn Pro Ser Ala Asp Asn Leu Tyr Lys Pro Ser Thr Asp Thr
180 185 190

Glu Glu Thr Glu Glu Glu Ala Glu Asp Thr Thr Asp Glu Ala Glu Ile
195 200 205

Pro Gly Thr Pro Ser Ile Arg Gln Asn Ala Met Glu Thr Leu Thr Gly
210 215 220

Leu Lys Ser Ser Leu Leu Leu Gly Thr Lys Asp Asn Asn Thr Ile Ser
225 230 235 240

Ala Glu Val Asp Ser Leu Leu Ala Leu Leu Lys Glu Ser Gln Pro Ala
245 250 255

Pro Ile Gln

<210> 375

<211> 268

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<400> 375

Met Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala
1 5 10 15

Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Thr Ser Trp Ile
20 25 30

Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr
35 40 45

Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser
50 55 60

Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys
65 70 75 80

Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr
85 90 95

Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro Pro Gly Asn Ile
100 105 110

Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala Pro Lys Gly Tyr
115 120 125

Ser Leu Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr Val Glu Pro Arg
130 135 140

Asn Ala Ser Asp His Val Arg Lys Asn Lys Ala Asp Gln Asp Ser Lys
145 150 155 160

Pro Asp Glu Asp Lys Glu His Asp Glu Val Ser Glu Pro Thr His Pro
165 170 175

Glu Ser Asp Glu Lys Glu Asn His Ala Gly Leu Asn Pro Ser Ala Asp
180 185 190

Asn Leu Tyr Lys Pro Ser Thr Asp Thr Glu Glu Thr Glu Glu Glu Ala
195 200 205

Glu Asp Thr Thr Asp Glu Ala Glu Ile Pro Gly Thr Pro Ser Ile Arg
210 215 220

Gln Asn Ala Met Glu Thr Leu Thr Gly Leu Lys Ser Ser Leu Leu Leu
225 230 235 240

Gly Thr Lys Asp Asn Asn Thr Ile Ser Ala Glu Val Asp Ser Leu Leu
245 250 255

Ala Leu Leu Lys Glu Ser Gln Pro Ala Pro Ile Gln
260 265

<210> 376

<211> .999

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<220>
 <221> MISC_FEATURE
 <222> (1)..(1)
 <223> Xaa = Methionine or nothing

<220>
 <221> MISC_FEATURE
 <222> (430)..(430)
 <223> Xaa = Glycine or nothing

<220>
 <221> MISC_FEATURE
 <222> (431)..(431)
 <223> Xaa = Proline or nothing

<400> 376

Xaa Asp Ile Asp Ser Leu Leu Lys Gln Leu Tyr Lys Leu Pro Leu Ser
 1 5 10 15

Gln Arg His Val Glu Ser Asp Gly Leu Ile Phe Asp Pro Ala Gln Ile
 20 25 30

Thr Ser Arg Thr Ala Arg Gly Val Ala Val Pro His Gly Asn His Tyr
 35 40 45

His Phe Ile Pro Tyr Glu Gln Met Ser Glu Leu Glu Lys Arg Ile Ala
 50 55 60

Arg Ile Ile Pro Leu Arg Tyr Arg Ser Asn His Trp Val Pro Asp Ser
 65 70 75 80

Arg Pro Glu Glu Pro Ser Pro Gln Pro Thr Pro Glu Pro Ser Pro Ser
 85 90 95

Pro Gln Pro Ala Pro Asn Pro Gln Pro Ala Pro Ser Asn Pro Ile Asp
 100 105 110

Glu Lys Leu Val Lys Glu Ala Val Arg Lys Val Gly Asp Gly Tyr Val
 115 120 125

Phe Glu Glu Asn Gly Val Ser Arg Tyr Ile Pro Ala Lys Asn Leu Ser
 130 135 140

Ala Glu Thr Ala Ala Gly Ile Asp Ser Lys Leu Ala Lys Gln Glu Ser

145

150

155

160

Leu Ser His Lys Leu Gly Ala Lys Lys Thr Asp Leu Pro Ser Ser Asp
 165 170 175

Arg Glu Phe Tyr Asn Lys Ala Tyr Asp Leu Leu Ala Arg Ile His Gln
 180 185 190

Asp Leu Leu Asp Asn Lys Gly Arg Gln Val Asp Phe Glu Ala Leu Asp
 195 200 205

Asn Leu Leu Glu Arg Leu Lys Asp Val Ser Ser Asp Lys Val Lys Leu
 210 215 220

Val Asp Asp Ile Leu Ala Phe Leu Ala Pro Ile Arg His Pro Glu Arg
 225 230 235 240

Leu Gly Lys Pro Asn Ala Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln
 245 250 255

Val Ala Lys Leu Ala Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe
 260 265 270

Asp Pro Arg Asp Ile Thr Ser Asp Glu Gly Asp Ala Tyr Val Thr Pro
 275 280 285

His Met Thr His Ser His Trp Ile Lys Lys Asp Ser Leu Ser Glu Ala
 290 295 300

Glu Arg Ala Ala Ala Gln Ala Tyr Ala Lys Glu Lys Gly Leu Thr Pro
 305 310 315 320

Pro Ser Thr Asp His Gln Asp Ser Gly Asn Thr Glu Ala Lys Gly Ala
 325 330 335

Glu Ala Ile Tyr Asn Arg Val Lys Ala Ala Lys Lys Val Pro Leu Asp
 340 345 350

Arg Met Pro Tyr Asn Leu Gln Tyr Thr Val Glu Val Lys Asn Gly Ser
 355 360 365

Leu Ile Ile Pro His Tyr Asp His Tyr His Asn Ile Lys Phe Glu Trp
 370 375 380

Phe Asp Glu Gly Leu Tyr Glu Ala Pro Lys Gly Tyr Thr Leu Glu Asp
385 390 395 400

Leu Leu Ala Thr Val Lys Tyr Tyr Val Glu His Pro Asn Glu Arg Pro
405 410 415

His Ser Asp Asn Gly Phe Gly Asn Ala Ser Asp His Val Xaa Xaa Asp
420 425 430

Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu Glu Val
435 440 445

Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser His Glu Gln Asp
450 455 460

Tyr Pro Gly Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys Ile Glu
465 470 475 480

Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg Glu Ser
485 490 495

Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro His Gly Asp
500 505 510

His His His Ala Asp Pro Ile Asp Glu His Lys Pro Val Gly Ile Gly
515 520 525

His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly Val Ala
530 535 540

Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr Asn Val
545 550 555 560

Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe Thr Leu
565 570 575

Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro Glu Leu Glu
580 585 590

Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr Pro Asp Gly
595 600 605

Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu Gly Val Gly
610 615 620

Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly Gln Thr
625 630 635 640

Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser Tyr Asp
645 650 655

Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala Ser Gln
660 665 670

Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg Val Asn
675 680 685

Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg Val Phe
690 695 700

Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys Val Gly
705 710 715 720

Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr Arg Thr
725 730 735

Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala Tyr Leu Asp
740 745 750

Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu Glu Lys Glu Asn
755 760 765

Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn Lys Ala
770 775 780

Gln Glu Asn Ser Lys Leu Asp Glu Lys Val Glu Glu Pro Lys Thr Ser
785 790 795 800

Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser Thr Ser
805 810 815

Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro Val Gln Glu Lys
820 825 830

Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn Val Leu
835 840 845

Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly Glu Val
850 855 860

Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala Pro Gln Gly Asn
865 870 875 880

Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser Thr Gly Thr Val
885 890 895

Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro Glu Ala
900 905 910

Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn Gly Met
915 920 925

Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp Pro Ala
930 935 940

Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu Glu Lys
945 950 955 960

Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe Asn Met
965 970 975

Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val Ile Lys Lys
980 985 990

Asn Leu Ser Asp Phe Ile Ala
995

<210> 377

<211> 999

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> Xaa = Methionine or nothing

<220>
<221> MISC_FEATURE
<222> (570)..(570)
<223> Xaa = Glycine or nothing

<220>
<221> MISC_FEATURE
<222> (571)..(571)
<223> Xaa = Proine or nothing

<400> 377

Xaa Asp Leu Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu
1 5 10 15

Glu Val Lys Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser His Glu
20 25 30

Gln Asp Tyr Pro Gly Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys
35 40 45

Ile Glu Glu Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg
50 55 60

Glu Ser Ile Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro His
65 70 75 80

Gly Asp His His His Ala Asp Pro Ile Asp Glu His Lys Pro Val Gly
85 90 95

Ile Gly His Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly
100 105 110

Val Ala Lys Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr
115 120 125

Asn Val Val Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe
130 135 140

Thr Leu Ala Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro Glu
145 150 155 160

Leu Glu Lys Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr Pro
165 170 175

Asp Gly Lys Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu Gly
180 185 190

Val Gly Asn Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly
195 200 205

Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser
210 215 220

Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala
225 230 235 240

Ser Gln Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg
245 250 255

Val Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg
260 265 270

Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys
275 280 285

Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr
290 295 300

Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala Tyr
305 310 315 320

Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu Glu Lys
325 330 335

Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn
340 345 350

Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys Val Glu Glu Pro Lys
355 360 365

Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser
370 375 380

Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro Val Gln
385 390 395 400

Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn
405 410 415

Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly
420 425 430

Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala Pro Gln
435 440 445

Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser Thr Gly
450 455 460

Thr Val Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro
465 470 475 480

Glu Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn
485 490 495

Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp
500 505 510

Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu
515 520 525

Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe
530 535 540

Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val Ile
545 550 555 560

Lys Lys Asn Leu Ser Asp Phe Ile Ala Xaa Xaa Asp Ile Asp Ser Leu
565 570 575

Leu Lys Gln Leu Tyr Lys Leu Pro Leu Ser Gln Arg His Val Glu Ser
580 585 590

Asp Gly Leu Ile Phe Asp Pro Ala Gln Ile Thr Ser Arg Thr Ala Arg
595 600 605

Gly Val Ala Val Pro His Gly Asn His Tyr His Phe Ile Pro Tyr Glu
610 615 620

Gln Met Ser Glu Leu Glu Lys Arg Ile Ala Arg Ile Ile Pro Leu Arg
625 630 635 640

Tyr Arg Ser Asn His Trp Val Pro Asp Ser Arg Pro Glu Glu Pro Ser
645 650 655

Pro Gln Pro Thr Pro Glu Pro Ser Pro Ser Pro Gln Pro Ala Pro Asn
660 665 670

Pro Gln Pro Ala Pro Ser Asn Pro Ile Asp Glu Lys Leu Val Lys Glu
675 680 685

Ala Val Arg Lys Val Gly Asp Gly Tyr Val Phe Glu Glu Asn Gly Val
690 695 700

Ser Arg Tyr Ile Pro Ala Lys Asn Leu Ser Ala Glu Thr Ala Ala Gly
705 710 715 720

Ile Asp Ser Lys Leu Ala Lys Gln Glu Ser Leu Ser His Lys Leu Gly
725 730 735

Ala Lys Lys Thr Asp Leu Pro Ser Ser Asp Arg Glu Phe Tyr Asn Lys
740 745 750

Ala Tyr Asp Leu Leu Ala Arg Ile His Gln Asp Leu Leu Asp Asn Lys
755 760 765

Gly Arg Gln Val Asp Phe Glu Ala Leu Asp Asn Leu Leu Glu Arg Leu
770 775 780

Lys Asp Val Ser Ser Asp Lys Val Lys Leu Val Asp Asp Ile Leu Ala
785 790 795 800

Phe Leu Ala Pro Ile Arg His Pro Glu Arg Leu Gly Lys Pro Asn Ala
805 810 815

Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala Gly
820 825 830

Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp Pro Arg Asp Ile Thr
835 840 845

Ser Asp Glu Gly Asp Ala Tyr Val Thr Pro His Met Thr His Ser His

850

855

860

Trp Ile Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln
865 870 875 880

Ala Tyr Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln
885 890 895

Asp Ser Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg
900 905 910

Val Lys Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu
915 920 925

Gln Tyr Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro His Tyr
930 935 940

Asp His Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr
945 950 955 960

Glu Ala Pro Lys Gly Tyr Thr Leu Glu Asp Leu Leu Ala Thr Val Lys
965 970 975

Tyr Tyr Val Glu His Pro Asn Glu Arg Pro His Ser Asp Asn Gly Phe
980 985 990

Gly Asn Ala Ser Asp His Val
995

<210> 378

<211> 1378

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> Xaa = Methionine or nothing

<220>

<221> MISC_FEATURE

<222> (570)..(570)

<223> Xaa = Glycine or nothing

<220>

<221> MISC_FEATURE

<222> (571)..(571)

<223> Xaa = Proline or nothing

<400> 378

Xaa Glu Asn Ile Ser Ser Leu Leu Arg Glu Leu Tyr Ala Lys Pro Leu
1 5 10 15

Ser Glu Arg His Val Glu Ser Asp Gly Leu Ile Phe Asp Pro Ala Gln
20 25 30

Ile Thr Ser Arg Thr Ala Arg Gly Val Ala Val Pro His Gly Asn His
35 40 45

Tyr His Phe Ile Pro Tyr Glu Gln Met Ser Glu Leu Glu Lys Arg Ile
50 55 60

Ala Arg Ile Ile Pro Leu Arg Tyr Arg Ser Asn His Trp Val Pro Asp
65 70 75 80

Ser Arg Pro Glu Gln Pro Ser Pro Gln Ser Thr Pro Glu Pro Ser Pro
85 90 95

Ser Leu Gln Pro Ala Pro Asn Pro Gln Pro Ala Pro Ser Asn Pro Ile
100 105 110

Asp Glu Lys Leu Val Lys Glu Ala Val Arg Lys Val Gly Asp Gly Tyr
115 120 125

Val Phe Glu Glu Asn Gly Val Ser Arg Tyr Ile Pro Ala Lys Asp Leu
130 135 140

Ser Ala Glu Thr Ala Ala Gly Ile Asp Ser Lys Leu Ala Lys Gln Glu
145 150 155 160

Ser Leu Ser His Lys Leu Gly Ala Lys Lys Thr Asp Leu Pro Ser Ser
165 170 175

Asp Arg Glu Phe Tyr Asn Lys Ala Tyr Asp Leu Leu Ala Arg Ile His
180 185 190

Gln Asp Leu Leu Asp Asn Lys Gly Arg Gln Val Asp Phe Glu Val Leu
195 200 205

Asp Asn Leu Leu Glu Arg Leu Lys Asp Val Ser Ser Asp Lys Val Lys
210 215 220

Leu Val Asp Asp Ile Leu Ala Phe Leu Ala Pro Ile Arg His Pro Glu
225 230 235 240

Arg Leu Gly Lys Pro Asn Ala Gln Ile Thr Tyr Thr Asp Asp Glu Ile
245 250 255

Gln Val Ala Lys Leu Ala Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile
260 265 270

Phe Asp Pro Arg Asp Ile Thr Ser Asp Glu Gly Asp Ala Tyr Val Thr
275 280 285

Pro His Met Thr His Ser His Trp Ile Lys Lys Asp Ser Leu Ser Glu
290 295 300

Ala Glu Arg Ala Ala Ala Gln Ala Tyr Ala Lys Glu Lys Gly Leu Thr
305 310 315 320

Pro Pro Ser Thr Asp His Gln Asp Ser Gly Asn Thr Glu Ala Lys Gly
325 330 335

Ala Glu Ala Ile Tyr Asn Arg Val Lys Ala Ala Lys Lys Val Pro Leu
340 345 350

Asp Arg Met Pro Tyr Asn Leu Gln Tyr Thr Val Glu Val Lys Asn Gly
355 360 365

Ser Leu Ile Ile Pro His Tyr Asp His Tyr His Asn Ile Lys Phe Glu
370 375 380

Trp Phe Asp Glu Gly Leu Tyr Glu Ala Pro Lys Gly Tyr Ser Leu Glu
385 390 395 400

Asp Leu Leu Ala Thr Val Lys Tyr Tyr Val Glu His Pro Asn Glu Arg
405 410 415

Pro His Ser Asp Asn Gly Phe Gly Asn Ala Ser Asp His Val Arg Lys
420 425 430

Asn Lys Ala Asp Gln Asp Ser Lys Pro Asp Glu Asp Lys Glu His Asp
435 440 445

Glu Val Ser Glu Pro Thr His Pro Glu Ser Asp Glu Lys Glu Asn His
450 455 460

Ala Gly Leu Asn Pro Ser Ala Asp Asn Leu Tyr Lys Pro Ser Thr Asp
465 470 475 480

Thr Glu Glu Thr Glu Glu Glu Ala Glu Asp Thr Thr Asp Glu Ala Glu
485 490 495

Ile Pro Gln Val Glu Asn Ser Val Ile Asn Ala Lys Ile Ala Asp Ala
500 505 510

Glu Ala Leu Leu Glu Lys Val Thr Asp Pro Ser Ile Arg Gln Asn Ala
515 520 525

Met Glu Thr Leu Thr Gly Leu Lys Ser Ser Leu Leu Leu Gly Thr Lys
530 535 540

Asp Asn Asn Thr Ile Ser Ala Glu Val Asp Ser Leu Leu Ala Leu Leu
545 550 555 560

Lys Glu Ser Gln Pro Ala Pro Ile Gln Xaa Xaa Asn Met Gln Pro Ser
565 570 575

Gln Leu Ser Tyr Ser Ser Thr Ala Ser Asp Asn Asn Thr Gln Ser Val
580 585 590

Ala Lys Gly Ser Thr Ser Lys Pro Ala Asn Lys Ser Glu Asn Leu Gln
595 600 605

Ser Leu Leu Lys Glu Leu Tyr Asp Ser Pro Ser Ala Gln Arg Tyr Ser
610 615 620

Glu Ser Asp Gly Leu Val Phe Asp Pro Ala Lys Ile Ile Ser Arg Thr
625 630 635 640

Pro Asn Gly Val Ala Ile Pro His Gly Asp His Tyr His Phe Ile Pro

645

650

655

Tyr Ser Lys Leu Ser Ala Leu Glu Glu Lys Ile Ala Arg Met Val Pro
660 665 670

Ile Ser Gly Thr Gly Ser Thr Val Ser Thr Asn Ala Lys Pro Asn Glu
675 680 685

Val Val Ser Ser Leu Gly Ser Leu Ser Ser Asn Pro Ser Ser Leu Thr
690 695 700

Thr Ser Lys Glu Leu Ser Ser Ala Ser Asp Gly Tyr Ile Phe Asn Pro
705 710 715 720

Lys Asp Ile Val Glu Glu Thr Ala Thr Ala Tyr Ile Val Arg His Gly
725 730 735

Asp His Phe His Tyr Ile Pro Lys Ser Asn Gln Ile Gly Gln Pro Thr
740 745 750

Leu Pro Asn Asn Ser Leu Ala Thr Pro Ser Pro Ser Leu Pro Ile Asn
755 760 765

Pro Gly Thr Ser His Glu Lys His Glu Glu Asp Gly Tyr Gly Phe Asp
770 775 780

Ala Asn Arg Ile Ile Ala Glu Asp Glu Ser Gly Phe Val Met Ser His
785 790 795 800

Gly Asp His Asn His Tyr Phe Phe Lys Lys Asp Leu Thr Glu Glu Gln
805 810 815

Ile Lys Ala Ala Gln Lys His Leu Glu Glu Val Lys Thr Ser His Asn
820 825 830

Gly Leu Asp Ser Leu Ser Ser His Glu Gln Asp Tyr Pro Gly Asn Ala
835 840 845

Lys Glu Met Lys Asp Leu Asp Lys Lys Ile Glu Glu Lys Ile Ala Gly
850 855 860

Ile Met Lys Gln Tyr Gly Val Lys Arg Glu Ser Ile Val Val Asn Lys
865 870 875 880

Glu Lys Asn Ala Ile Ile Tyr Pro His Gly Asp His His His Ala Asp
885 890 895

Pro Ile Asp Glu His Lys Pro Val Gly Ile Gly His Ser His Ser Asn
900 905 910

Tyr Glu Leu Phe Lys Pro Glu Glu Gly Val Ala Lys Lys Glu Gly Asn
915 920 925

Lys Val Tyr Thr Gly Glu Glu Leu Thr Asn Val Val Asn Leu Leu Lys
930 935 940

Asn Ser Thr Phe Asn Asn Gln Asn Phe Thr Leu Ala Asn Gly Gln Lys
945 950 955 960

Arg Val Ser Phe Ser Phe Pro Pro Glu Leu Glu Lys Lys Leu Gly Ile
965 970 975

Asn Met Leu Val Lys Leu Ile Thr Pro Asp Gly Lys Val Leu Glu Lys
980 985 990

Val Ser Gly Lys Val Phe Gly Glu Gly Val Gly Asn Ile Ala Asn Phe
995 1000 1005

Glu Leu Asp Gln Pro Tyr Leu Pro Gly Gln Thr Phe Lys Tyr Thr
1010 1015 1020

Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser Tyr Asp Gly Thr Phe
1025 1030 1035

Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala Ser Gln Thr Ile
1040 1045 1050

Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg Val Asn Pro
1055 1060 1065

Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg Val Phe
1070 1075 1080

Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys Val
1085 1090 1095

Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr
1100 1105 1110

Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala
1115 1120 1125

Tyr Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu
1130 1135 1140

Glu Lys Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe
1145 1150 1155

Lys Arg Asn Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu Lys Val
1160 1165 1170

Glu Glu Pro Lys Thr Ser Glu Lys Val Glu Lys Glu Lys Leu Ser
1175 1180 1185

Glu Thr Gly Asn Ser Thr Ser Asn Ser Thr Leu Glu Glu Val Pro
1190 1195 1200

Thr Val Asp Pro Val Gln Glu Lys Val Ala Lys Phe Ala Glu Ser
1205 1210 1215

Tyr Gly Met Lys Leu Glu Asn Val Leu Phe Asn Met Asp Gly Thr
1220 1225 1230

Ile Glu Leu Tyr Leu Pro Ser Gly Glu Val Ile Lys Lys Asn Met
1235 1240 1245

Ala Asp Phe Thr Gly Glu Ala Pro Gln Gly Asn Gly Glu Asn Lys
1250 1255 1260

Pro Ser Glu Asn Gly Lys Val Ser Thr Gly Thr Val Glu Asn Gln
1265 1270 1275

Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro Glu Ala Pro Asn
1280 1285 1290

Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn Gly Met Leu
1295 1300 1305

Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp Pro Ala
1310 1315 1320

Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu Glu
1325 1330 1335

Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe
1340 1345 1350

Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val
1355 1360 1365

Ile Lys Lys Asn Leu Ser Asp Phe Ile Ala
1370 1375

<210> 379
<211> 1152
<212> PRT
<213> Artificial Sequence

<220>
<223> Unknown Organism

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa = Methionine or nothing

<220>
<221> MISC_FEATURE
<222> (344)..(344)
<223> Xaa = Glycine or nothing

<220>
<221> MISC_FEATURE
<222> (345)..(345)
<223> Xaa = Proline or nothing

<400> 379

Xaa Asp Ile Leu Ala Phe Leu Ala Pro Ile Arg His Pro Glu Arg Leu
1 5 10 15

Gly Lys Pro Asn Ala Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val
20 25 30

Ala Lys Leu Ala Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp

35

40

45

Pro Arg Asp Ile Thr Ser Asp Glu Gly Asp Ala Tyr Val Thr Pro His
50 55 60

Met Thr His Ser His Trp Ile Lys Lys Asp Ser Leu Ser Glu Ala Glu
65 70 75 80

Arg Ala Ala Ala Gln Ala Tyr Ala Lys Glu Lys Gly Leu Thr Pro Pro
85 90 95

Ser Thr Asp His Gln Asp Ser Gly Asn Thr Glu Ala Lys Gly Ala Glu
100 105 110

Ala Ile Tyr Asn Arg Val Lys Ala Ala Lys Lys Val Pro Leu Asp Arg
115 120 125

Met Pro Tyr Asn Leu Gln Tyr Thr Val Glu Val Lys Asn Gly Ser Leu
130 135 140

Ile Ile Pro His Tyr Asp His Tyr His Asn Ile Lys Phe Glu Trp Phe
145 150 155 160

Asp Glu Gly Leu Tyr Glu Ala Pro Lys Gly Tyr Ser Leu Glu Asp Leu
165 170 175

Leu Ala Thr Val Lys Tyr Tyr Val Glu His Pro Asn Glu Arg Pro His
180 185 190

Ser Asp Asn Gly Phe Gly Asn Ala Ser Asp His Val Arg Lys Asn Lys
195 200 205

Ala Asp Gln Asp Ser Lys Pro Asp Glu Asp Lys Glu His Asp Glu Val
210 215 220

Ser Glu Pro Thr His Pro Glu Ser Asp Glu Lys Glu Asn His Ala Gly
225 230 235 240

Leu Asn Pro Ser Ala Asp Asn Leu Tyr Lys Pro Ser Thr Asp Thr Glu
245 250 255

Glu Thr Glu Glu Glu Ala Glu Asp Thr Thr Asp Glu Ala Glu Ile Pro
260 265 270

Gln Val Glu Asn Ser Val Ile Asn Ala Lys Ile Ala Asp Ala Glu Ala
275 280 285

Leu Leu Glu Lys Val Thr Asp Pro Ser Ile Arg Gln Asn Ala Met Glu
290 295 300

Thr Leu Thr Gly Leu Lys Ser Ser Leu Leu Leu Gly Thr Lys Asp Asn
305 310 315 320

Asn Thr Ile Ser Ala Glu Val Asp Ser Leu Leu Ala Leu Leu Lys Glu
325 330 335

Ser Gln Pro Ala Pro Ile Gln Xaa Xaa Asn Met Gln Pro Ser Gln Leu
340 345 350

Ser Tyr Ser Ser Thr Ala Ser Asp Asn Asn Thr Gln Ser Val Ala Lys
355 360 365

Gly Ser Thr Ser Lys Pro Ala Asn Lys Ser Glu Asn Leu Gln Ser Leu
370 375 380

Leu Lys Glu Leu Tyr Asp Ser Pro Ser Ala Gln Arg Tyr Ser Glu Ser
385 390 395 400

Asp Gly Leu Val Phe Asp Pro Ala Lys Ile Ile Ser Arg Thr Pro Asn
405 410 415

Gly Val Ala Ile Pro His Gly Asp His Tyr His Phe Ile Pro Tyr Ser
420 425 430

Lys Leu Ser Ala Leu Glu Glu Lys Ile Ala Arg Met Val Pro Ile Ser
435 440 445

Gly Thr Gly Ser Thr Val Ser Thr Asn Ala Lys Pro Asn Glu Val Val
450 455 460

Ser Ser Leu Gly Ser Leu Ser Ser Asn Pro Ser Ser Leu Thr Thr Ser
465 470 475 480

Lys Glu Leu Ser Ser Ala Ser Asp Gly Tyr Ile Phe Asn Pro Lys Asp
485 490 495

Ile Val Glu Glu Thr Ala Thr Ala Tyr Ile Val Arg His Gly Asp His
500 505 510

Phe His Tyr Ile Pro Lys Ser Asn Gln Ile Gly Gln Pro Thr Leu Pro
515 520 525

Asn Asn Ser Leu Ala Thr Pro Ser Pro Ser Leu Pro Ile Asn Pro Gly
530 535 540

Thr Ser His Glu Lys His Glu Glu Asp Gly Tyr Gly Phe Asp Ala Asn
545 550 555 560

Arg Ile Ile Ala Glu Asp Glu Ser Gly Phe Val Met Ser His Gly Asp
565 570 575

His Asn His Tyr Phe Phe Lys Lys Asp Leu Thr Glu Glu Gln Ile Lys
580 585 590

Ala Ala Gln Lys His Leu Glu Glu Val Lys Thr Ser His Asn Gly Leu
595 600 605

Asp Ser Leu Ser Ser His Glu Gln Asp Tyr Pro Gly Asn Ala Lys Glu
610 615 620

Met Lys Asp Leu Asp Lys Lys Ile Glu Glu Lys Ile Ala Gly Ile Met
625 630 635 640

Lys Gln Tyr Gly Val Lys Arg Glu Ser Ile Val Val Asn Lys Glu Lys
645 650 655

Asn Ala Ile Ile Tyr Pro His Gly Asp His His His Ala Asp Pro Ile
660 665 670

Asp Glu His Lys Pro Val Gly Ile Gly His Ser His Ser Asn Tyr Glu
675 680 685

Leu Phe Lys Pro Glu Glu Gly Val Ala Lys Lys Glu Gly Asn Lys Val
690 695 700

Tyr Thr Gly Glu Glu Leu Thr Asn Val Val Asn Leu Leu Lys Asn Ser
705 710 715 720

Thr Phe Asn Asn Gln Asn Phe Thr Leu Ala Asn Gly Gln Lys Arg Val
725 730 735

Ser Phe Ser Phe Pro Pro Glu Leu Glu Lys Lys Leu Gly Ile Asn Met
740 745 750

Leu Val Lys Leu Ile Thr Pro Asp Gly Lys Val Leu Glu Lys Val Ser
755 760 765

Gly Lys Val Phe Gly Glu Gly Val Gly Asn Ile Ala Asn Phe Glu Leu
770 775 780

Asp Gln Pro Tyr Leu Pro Gly Gln Thr Phe Lys Tyr Thr Ile Ala Ser
785 790 795 800

Lys Asp Tyr Pro Glu Val Ser Tyr Asp Gly Thr Phe Thr Val Pro Thr
805 810 815

Ser Leu Ala Tyr Lys Met Ala Ser Gln Thr Ile Phe Tyr Pro Phe His
820 825 830

Ala Gly Asp Thr Tyr Leu Arg Val Asn Pro Gln Phe Ala Val Pro Lys
835 840 845

Gly Thr Asp Ala Leu Val Arg Val Phe Asp Glu Phe His Gly Asn Ala
850 855 860

Tyr Leu Glu Asn Asn Tyr Lys Val Gly Glu Ile Lys Leu Pro Ile Pro
865 870 875 880

Lys Leu Asn Gln Gly Thr Thr Arg Thr Ala Gly Asn Lys Ile Pro Val
885 890 895

Thr Phe Met Ala Asn Ala Tyr Leu Asp Asn Gln Ser Thr Tyr Ile Val
900 905 910

Glu Val Pro Ile Leu Glu Lys Glu Asn Gln Thr Asp Lys Pro Ser Ile
915 920 925

Leu Pro Gln Phe Lys Arg Asn Lys Ala Gln Glu Asn Ser Lys Leu Asp
930 935 940

Glu Lys Val Glu Glu Pro Lys Thr Ser Glu Lys Val Glu Lys Glu Lys

945

950

955

960

Leu Ser Glu Thr Gly Asn Ser Thr Ser Asn Ser Thr Leu Glu Glu Val
 965 970 975

Pro Thr Val Asp Pro Val Gln Glu Lys Val Ala Lys Phe Ala Glu Ser
 980 985 990

Tyr Gly Met Lys Leu Glu Asn Val Leu Phe Asn Met Asp Gly Thr Ile
 995 1000 1005

Glu Leu Tyr Leu Pro Ser Gly Glu Val Ile Lys Lys Asn Met Ala
 1010 1015 1020

Asp Phe Thr Gly Glu Ala Pro Gln Gly Asn Gly Glu Asn Lys Pro
 1025 1030 1035

Ser Glu Asn Gly Lys Val Ser Thr Gly Thr Val Glu Asn Gln Pro
 1040 1045 1050

Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro Glu Ala Pro Asn Glu
 1055 1060 1065

Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn Gly Met Leu Asn
 1070 1075 1080

Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp Pro Ala Leu
 1085 1090 1095

Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu Glu Lys
 1100 1105 1110

Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile Phe Asn
 1115 1120 1125

Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu Val Ile
 1130 1135 1140

Lys Lys Asn Leu Ser Asp Phe Ile Ala
 1145 1150

<210> 380

<211> 1139

<212> PRT
<213> Artificial Sequence

<220>
<223> Unknown Organism

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa = Methionine or nothing

<220>
<221> MISC_FEATURE
<222> (570)..(570)
<223> Xaa = Glycine or nothing

<220>
<221> MISC_FEATURE
<222> (571)..(571)
<223> Xaa = Proline or nothing

<400> 380

Xaa Glu Asn Ile Ser Ser Leu Leu Arg Glu Leu Tyr Ala Lys Pro Leu
1 5 10 15

Ser Glu Arg His Val Glu Ser Asp Gly Leu Ile Phe Asp Pro Ala Gln
20 25 30

Ile Thr Ser Arg Thr Ala Arg Gly Val Ala Val Pro His Gly Asn His
35 40 45

Tyr His Phe Ile Pro Tyr Glu Gln Met Ser Glu Leu Glu Lys Arg Ile
50 55 60

Ala Arg Ile Ile Pro Leu Arg Tyr Arg Ser Asn His Trp Val Pro Asp
65 70 75 80

Ser Arg Pro Glu Gln Pro Ser Pro Gln Ser Thr Pro Glu Pro Ser Pro
85 90 95

Ser Leu Gln Pro Ala Pro Asn Pro Gln Pro Ala Pro Ser Asn Pro Ile
100 105 110

Asp Glu Lys Leu Val Lys Glu Ala Val Arg Lys Val Gly Asp Gly Tyr
115 120 125

Val Phe Glu Glu Asn Gly Val Ser Arg Tyr Ile Pro Ala Lys Asp Leu
130 135 140

Ser Ala Glu Thr Ala Ala Gly Ile Asp Ser Lys Leu Ala Lys Gln Glu
145 150 155 160

Ser Leu Ser His Lys Leu Gly Ala Lys Lys Thr Asp Leu Pro Ser Ser
165 170 175

Asp Arg Glu Phe Tyr Asn Lys Ala Tyr Asp Leu Leu Ala Arg Ile His
180 185 190

Gln Asp Leu Leu Asp Asn Lys Gly Arg Gln Val Asp Phe Glu Val Leu
195 200 205

Asp Asn Leu Leu Glu Arg Leu Lys Asp Val Ser Ser Asp Lys Val Lys
210 215 220

Leu Val Asp Asp Ile Leu Ala Phe Leu Ala Pro Ile Arg His Pro Glu
225 230 235 240

Arg Leu Gly Lys Pro Asn Ala Gln Ile Thr Tyr Thr Asp Asp Glu Ile
245 250 255

Gln Val Ala Lys Leu Ala Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile
260 265 270

Phe Asp Pro Arg Asp Ile Thr Ser Asp Glu Gly Asp Ala Tyr Val Thr
275 280 285

Pro His Met Thr His Ser His Trp Ile Lys Lys Asp Ser Leu Ser Glu
290 295 300

Ala Glu Arg Ala Ala Ala Gln Ala Tyr Ala Lys Glu Lys Gly Leu Thr
305 310 315 320

Pro Pro Ser Thr Asp His Gln Asp Ser Gly Asn Thr Glu Ala Lys Gly
325 330 335

Ala Glu Ala Ile Tyr Asn Arg Val Lys Ala Ala Lys Lys Val Pro Leu
340 345 350

Asp Arg Met Pro Tyr Asn Leu Gln Tyr Thr Val Glu Val Lys Asn Gly
355 360 365

Ser Leu Ile Ile Pro His Tyr Asp His Tyr His Asn Ile Lys Phe Glu
370 375 380

Trp Phe Asp Glu Gly Leu Tyr Glu Ala Pro Lys Gly Tyr Ser Leu Glu
385 390 395 400

Asp Leu Leu Ala Thr Val Lys Tyr Tyr Val Glu His Pro Asn Glu Arg
405 410 415

Pro His Ser Asp Asn Gly Phe Gly Asn Ala Ser Asp His Val Arg Lys
420 425 430

Asn Lys Ala Asp Gln Asp Ser Lys Pro Asp Glu Asp Lys Glu His Asp
435 440 445

Glu Val Ser Glu Pro Thr His Pro Glu Ser Asp Glu Lys Glu Asn His
450 455 460

Ala Gly Leu Asn Pro Ser Ala Asp Asn Leu Tyr Lys Pro Ser Thr Asp
465 470 475 480

Thr Glu Glu Thr Glu Glu Glu Ala Glu Asp Thr Thr Asp Glu Ala Glu
485 490 495

Ile Pro Gln Val Glu Asn Ser Val Ile Asn Ala Lys Ile Ala Asp Ala
500 505 510

Glu Ala Leu Leu Glu Lys Val Thr Asp Pro Ser Ile Arg Gln Asn Ala
515 520 525

Met Glu Thr Leu Thr Gly Leu Lys Ser Ser Leu Leu Leu Gly Thr Lys
530 535 540

Asp Asn Asn Thr Ile Ser Ala Glu Val Asp Ser Leu Leu Ala Leu Leu
545 550 555 560

Lys Glu Ser Gln Pro Ala Pro Ile Gln Xaa Xaa Asp Leu Thr Glu Glu
565 570 575

Gln Ile Lys Ala Ala Gln Lys His Leu Glu Glu Val Lys Thr Ser His

580

585

590

Asn Gly Leu Asp Ser Leu Ser Ser His Glu Gln Asp Tyr Pro Gly Asn
 595 600 605

Ala Lys Glu Met Lys Asp Leu Asp Lys Lys Ile Glu Glu Lys Ile Ala
 610 615 620

Gly Ile Met Lys Gln Tyr Gly Val Lys Arg Glu Ser Ile Val Val Asn
 625 630 635 640

Lys Glu Lys Asn Ala Ile Ile Tyr Pro His Gly Asp His His His Ala
 645 650 655

Asp Pro Ile Asp Glu His Lys Pro Val Gly Ile Gly His Ser His Ser
 660 665 670

Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly Val Ala Lys Lys Glu Gly
 675 680 685

Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr Asn Val Val Asn Leu Leu
 690 695 700

Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe Thr Leu Ala Asn Gly Gln
 705 710 715 720

Lys Arg Val Ser Phe Ser Phe Pro Pro Glu Leu Glu Lys Lys Leu Gly
 725 730 735

Ile Asn Met Leu Val Lys Leu Ile Thr Pro Asp Gly Lys Val Leu Glu
 740 745 750

Lys Val Ser Gly Lys Val Phe Gly Glu Gly Val Gly Asn Ile Ala Asn
 755 760 765

Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly Gln Thr Phe Lys Tyr Thr
 770 775 780

Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser Tyr Asp Gly Thr Phe Thr
 785 790 795 800

Val Pro Thr Ser Leu Ala Tyr Lys Met Ala Ser Gln Thr Ile Phe Tyr
 805 810 815

Pro Phe His Ala Gly Asp Thr Tyr Leu Arg Val Asn Pro Gln Phe Ala
820 825 830

Val Pro Lys Gly Thr Asp Ala Leu Val Arg Val Phe Asp Glu Phe His
835 840 845

Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys Val Gly Glu Ile Lys Leu
850 855 860

Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr Arg Thr Ala Gly Asn Lys
865 870 875 880

Ile Pro Val Thr Phe Met Ala Asn Ala Tyr Leu Asp Asn Gln Ser Thr
885 890 895

Tyr Ile Val Glu Val Pro Ile Leu Glu Lys Glu Asn Gln Thr Asp Lys
900 905 910

Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn Lys Ala Gln Glu Asn Ser
915 920 925

Lys Leu Asp Glu Lys Val Glu Glu Pro Lys Thr Ser Glu Lys Val Glu
930 935 940

Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser Thr Ser Asn Ser Thr Leu
945 950 955 960

Glu Glu Val Pro Thr Val Asp Pro Val Gln Glu Lys Val Ala Lys Phe
965 970 975

Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn Val Leu Phe Asn Met Asp
980 985 990

Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly Glu Val Ile Lys Lys Asn
995 1000 1005

Met Ala Asp Phe Thr Gly Glu Ala Pro Gln Gly Asn Gly Glu Asn
1010 1015 1020

Lys Pro Ser Glu Asn Gly Lys Val Ser Thr Gly Thr Val Glu Asn
1025 1030 1035

Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro Glu Ala Pro
1040 1045 1050

Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn Gly Met
1055 1060 1065

Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp Pro
1070 1075 1080

Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys Leu
1085 1090 1095

Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val Ile
1100 1105 1110

Phe Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly Glu
1115 1120 1125

Val Ile Lys Lys Asn Leu Ser Asp Phe Ile Ala
1130 1135

<210> 381
<211> 1238
<212> PRT
<213> Artificial Sequence

<220>
<223> Unknown Organism

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa = Methionine or nothing

<220>
<221> MISC_FEATURE
<222> (430)..(430)
<223> Xaa = Glycine or nothing

<220>
<221> MISC_FEATURE
<222> (431)..(431)
<223> Xaa = Proline or nothing

<400> 381

Xaa Asp Ile Asp Ser Leu Leu Lys Gln Leu Tyr Lys Leu Pro Leu Ser
1 5 10 15

Gln Arg His Val Glu Ser Asp Gly Leu Ile Phe Asp Pro Ala Gln Ile
20 25 30

Thr Ser Arg Thr Ala Arg Gly Val Ala Val Pro His Gly Asn His Tyr
35 40 45

His Phe Ile Pro Tyr Glu Gln Met Ser Glu Leu Glu Lys Arg Ile Ala
50 55 60

Arg Ile Ile Pro Leu Arg Tyr Arg Ser Asn His Trp Val Pro Asp Ser
65 70 75 80

Arg Pro Glu Glu Pro Ser Pro Gln Pro Thr Pro Glu Pro Ser Pro Ser
85 90 95

Pro Gln Pro Ala Pro Asn Pro Gln Pro Ala Pro Ser Asn Pro Ile Asp
100 105 110

Glu Lys Leu Val Lys Glu Ala Val Arg Lys Val Gly Asp Gly Tyr Val
115 120 125

Phe Glu Glu Asn Gly Val Ser Arg Tyr Ile Pro Ala Lys Asn Leu Ser
130 135 140

Ala Glu Thr Ala Ala Gly Ile Asp Ser Lys Leu Ala Lys Gln Glu Ser
145 150 155 160

Leu Ser His Lys Leu Gly Ala Lys Lys Thr Asp Leu Pro Ser Ser Asp
165 170 175

Arg Glu Phe Tyr Asn Lys Ala Tyr Asp Leu Leu Ala Arg Ile His Gln
180 185 190

Asp Leu Leu Asp Asn Lys Gly Arg Gln Val Asp Phe Glu Ala Leu Asp
195 200 205

Asn Leu Leu Glu Arg Leu Lys Asp Val Ser Ser Asp Lys Val Lys Leu
210 215 220

Val Asp Asp Ile Leu Ala Phe Leu Ala Pro Ile Arg His Pro Glu Arg

225		230		235		240
Leu Gly Lys Pro Asn Ala Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln						
	245			250		255
Val Ala Lys Leu Ala Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe						
	260		265			270
Asp Pro Arg Asp Ile Thr Ser Asp Glu Gly Asp Ala Tyr Val Thr Pro						
	275		280			285
His Met Thr His Ser His Trp Ile Lys Lys Asp Ser Leu Ser Glu Ala						
	290		295			300
Glu Arg Ala Ala Ala Gln Ala Tyr Ala Lys Glu Lys Gly Leu Thr Pro						
305		310		315		320
Pro Ser Thr Asp His Gln Asp Ser Gly Asn Thr Glu Ala Lys Gly Ala						
	325		330			335
Glu Ala Ile Tyr Asn Arg Val Lys Ala Ala Lys Lys Val Pro Leu Asp						
	340		345			350
Arg Met Pro Tyr Asn Leu Gln Tyr Thr Val Glu Val Lys Asn Gly Ser						
	355		360			365
Leu Ile Ile Pro His Tyr Asp His Tyr His Asn Ile Lys Phe Glu Trp						
	370		375			380
Phe Asp Glu Gly Leu Tyr Glu Ala Pro Lys Gly Tyr Thr Leu Glu Asp						
385		390		395		400
Leu Leu Ala Thr Val Lys Tyr Tyr Val Glu His Pro Asn Glu Arg Pro						
	405		410			415
His Ser Asp Asn Gly Phe Gly Asn Ala Ser Asp His Val Xaa Xaa Asn						
	420		425			430
Met Gln Pro Ser Gln Leu Ser Tyr Ser Ser Thr Ala Ser Asp Asn Asn						
	435		440			445
Thr Gln Ser Val Ala Lys Gly Ser Thr Ser Lys Pro Ala Asn Lys Ser						
	450		455			460

Glu Asn Leu Gln Ser Leu Leu Lys Glu Leu Tyr Asp Ser Pro Ser Ala
465 470 475 480

Gln Arg Tyr Ser Glu Ser Asp Gly Leu Val Phe Asp Pro Ala Lys Ile
485 490 495

Ile Ser Arg Thr Pro Asn Gly Val Ala Ile Pro His Gly Asp His Tyr
500 505 510

His Phe Ile Pro Tyr Ser Lys Leu Ser Ala Leu Glu Glu Lys Ile Ala
515 520 525

Arg Met Val Pro Ile Ser Gly Thr Gly Ser Thr Val Ser Thr Asn Ala
530 535 540

Lys Pro Asn Glu Val Val Ser Ser Leu Gly Ser Leu Ser Ser Asn Pro
545 550 555 560

Ser Ser Leu Thr Thr Ser Lys Glu Leu Ser Ser Ala Ser Asp Gly Tyr
565 570 575

Ile Phe Asn Pro Lys Asp Ile Val Glu Glu Thr Ala Thr Ala Tyr Ile
580 585 590

Val Arg His Gly Asp His Phe His Tyr Ile Pro Lys Ser Asn Gln Ile
595 600 605

Gly Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr Pro Ser Pro Ser
610 615 620

Leu Pro Ile Asn Pro Gly Thr Ser His Glu Lys His Glu Glu Asp Gly
625 630 635 640

Tyr Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp Glu Ser Gly Phe
645 650 655

Val Met Ser His Gly Asp His Asn His Tyr Phe Phe Lys Lys Asp Leu
660 665 670

Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu Glu Val Lys
675 680 685

Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser His Glu Gln Asp Tyr
690 695 700

Pro Gly Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys Ile Glu Glu
705 710 715 720

Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg Glu Ser Ile
725 730 735

Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro His Gly Asp His
740 745 750

His His Ala Asp Pro Ile Asp Glu His Lys Pro Val Gly Ile Gly His
755 760 765

Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly Val Ala Lys
770 775 780

Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr Asn Val Val
785 790 795 800

Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe Thr Leu Ala
805 810 815

Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro Glu Leu Glu Lys
820 825 830

Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr Pro Asp Gly Lys
835 840 845

Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu Gly Val Gly Asn
850 855 860

Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly Gln Thr Phe
865 870 875 880

Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser Tyr Asp Gly
885 890 895

Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala Ser Gln Thr
900 905 910

Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg Val Asn Pro
915 920 925

Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg Val Phe Asp
930 935 940

Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys Val Gly Glu
945 950 955 960

Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr Arg Thr Ala
965 970 975

Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala Tyr Leu Asp Asn
980 985 990

Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu Glu Lys Glu Asn Gln
995 1000 1005

Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn Lys Ala
1010 1015 1020

Gln Glu Asn Ser Lys Leu Asp Glu Lys Val Glu Glu Pro Lys Thr
1025 1030 1035

Ser Glu Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser
1040 1045 1050

Thr Ser Asn Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro Val
1055 1060 1065

Gln Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu
1070 1075 1080

Glu Asn Val Leu Phe Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu
1085 1090 1095

Pro Ser Gly Glu Val Ile Lys Lys Asn Met Ala Asp Phe Thr Gly
1100 1105 1110

Glu Ala Pro Gln Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn Gly
1115 1120 1125

Lys Val Ser Thr Gly Thr Val Glu Asn Gln Pro Thr Glu Asn Lys

1130		1135		1140
Pro Ala	Asp Ser Leu	Pro Glu	Ala Pro Asn Glu	Lys Pro Val Lys
1145		1150		1155
Pro Glu	Asn Ser Thr	Asp Asn	Gly Met Leu Asn	Pro Glu Gly Asn
1160		1165		1170
Val Gly	Ser Asp Pro Met	Leu Asp	Pro Ala Leu	Glu Glu Ala Pro
1175		1180		1185
Ala Val	Asp Pro Val Gln	Glu Lys	Leu Glu Lys	Phe Thr Ala Ser
1190		1195		1200
Tyr Gly	Leu Gly Leu Asp	Ser Val	Ile Phe Asn	Met Asp Gly Thr
1205		1210		1215
Ile Glu	Leu Arg Leu Pro	Ser Gly	Glu Val Ile	Lys Lys Asn Leu
1220		1225		1230
Ser Asp	Phe Ile Ala			
1235				

<210> 382
 <211> 1365
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Unknown Organism

<220>
 <221> MISC_FEATURE
 <222> (1)..(1)
 <223> Xaa = Methionine or nothing

<220>
 <221> MISC_FEATURE
 <222> (557)..(557)
 <223> Xaa = Glycine or nothing

<220>
 <221> MISC_FEATURE
 <222> (558)..(558)
 <223> Xaa = Proline or nothing

<400> 382

Xaa Asp Ile Asp Ser Leu Leu Lys Gln Leu Tyr Lys Leu Pro Leu Ser
1 5 10 15

Gln Arg His Val Glu Ser Asp Gly Leu Ile Phe Asp Pro Ala Gln Ile
20 25 30

Thr Ser Arg Thr Ala Arg Gly Val Ala Val Pro His Gly Asn His Tyr
35 40 45

His Phe Ile Pro Tyr Glu Gln Met Ser Glu Leu Glu Lys Arg Ile Ala
50 55 60

Arg Ile Ile Pro Leu Arg Tyr Arg Ser Asn His Trp Val Pro Asp Ser
65 70 75 80

Arg Pro Glu Glu Pro Ser Pro Gln Pro Thr Pro Glu Pro Ser Pro Ser
85 90 95

Pro Gln Pro Ala Pro Asn Pro Gln Pro Ala Pro Ser Asn Pro Ile Asp
100 105 110

Glu Lys Leu Val Lys Glu Ala Val Arg Lys Val Gly Asp Gly Tyr Val
115 120 125

Phe Glu Glu Asn Gly Val Ser Arg Tyr Ile Pro Ala Lys Asn Leu Ser
130 135 140

Ala Glu Thr Ala Ala Gly Ile Asp Ser Lys Leu Ala Lys Gln Glu Ser
145 150 155 160

Leu Ser His Lys Leu Gly Ala Lys Lys Thr Asp Leu Pro Ser Ser Asp
165 170 175

Arg Glu Phe Tyr Asn Lys Ala Tyr Asp Leu Leu Ala Arg Ile His Gln
180 185 190

Asp Leu Leu Asp Asn Lys Gly Arg Gln Val Asp Phe Glu Ala Leu Asp
195 200 205

Asn Leu Leu Glu Arg Leu Lys Asp Val Ser Ser Asp Lys Val Lys Leu
210 215 220

Val Asp Asp Ile Leu Ala Phe Leu Ala Pro Ile Arg His Pro Glu Arg
225 230 235 240

Leu Gly Lys Pro Asn Ala Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln
245 250 255

Val Ala Lys Leu Ala Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe
260 265 270

Asp Pro Arg Asp Ile Thr Ser Asp Glu Gly Asp Ala Tyr Val Thr Pro
275 280 285

His Met Thr His Ser His Trp Ile Lys Lys Asp Ser Leu Ser Glu Ala
290 295 300

Glu Arg Ala Ala Ala Gln Ala Tyr Ala Lys Glu Lys Gly Leu Thr Pro
305 310 315 320

Pro Ser Thr Asp His Gln Asp Ser Gly Asn Thr Glu Ala Lys Gly Ala
325 330 335

Glu Ala Ile Tyr Asn Arg Val Lys Ala Ala Lys Lys Val Pro Leu Asp
340 345 350

Arg Met Pro Tyr Asn Leu Gln Tyr Thr Val Glu Val Lys Asn Gly Ser
355 360 365

Leu Ile Ile Pro His Tyr Asp His Tyr His Asn Ile Lys Phe Glu Trp
370 375 380

Phe Asp Glu Gly Leu Tyr Glu Ala Pro Lys Gly Tyr Thr Leu Glu Asp
385 390 395 400

Leu Leu Ala Thr Val Lys Tyr Tyr Val Glu His Pro Asn Glu Arg Pro
405 410 415

His Ser Asp Asn Gly Phe Gly Asn Ala Ser Asp His Val Gln Arg Asn
420 425 430

Lys Asn Gly Gln Ala Asp Thr Asn Gln Thr Glu Lys Pro Ser Glu Glu
435 440 445

Lys Pro Gln Thr Glu Lys Pro Glu Glu Glu Thr Pro Arg Glu Glu Lys
450 455 460

Pro Gln Ser Glu Lys Pro Glu Ser Pro Lys Pro Thr Glu Glu Pro Glu
465 470 475 480

Glu Glu Ser Pro Glu Glu Ser Glu Glu Pro Gln Val Glu Thr Glu Lys
485 490 495

Val Glu Glu Lys Leu Arg Glu Ala Glu Asp Leu Leu Gly Lys Ile Gln
500 505 510

Asp Pro Ile Ile Lys Ser Asn Ala Lys Glu Thr Leu Thr Gly Leu Lys
515 520 525

Asn Asn Leu Leu Phe Gly Thr Gln Asp Asn Asn Thr Ile Met Ala Glu
530 535 540

Ala Glu Lys Leu Leu Ala Leu Leu Lys Glu Ser Lys Xaa Xaa Asn Met
545 550 555 560

Gln Pro Ser Gln Leu Ser Tyr Ser Ser Thr Ala Ser Asp Asn Asn Thr
565 570 575

Gln Ser Val Ala Lys Gly Ser Thr Ser Lys Pro Ala Asn Lys Ser Glu
580 585 590

Asn Leu Gln Ser Leu Leu Lys Glu Leu Tyr Asp Ser Pro Ser Ala Gln
595 600 605

Arg Tyr Ser Glu Ser Asp Gly Leu Val Phe Asp Pro Ala Lys Ile Ile
610 615 620

Ser Arg Thr Pro Asn Gly Val Ala Ile Pro His Gly Asp His Tyr His
625 630 635 640

Phe Ile Pro Tyr Ser Lys Leu Ser Ala Leu Glu Glu Lys Ile Ala Arg
645 650 655

Met Val Pro Ile Ser Gly Thr Gly Ser Thr Val Ser Thr Asn Ala Lys
660 665 670

Pro Asn Glu Val Val Ser Ser Leu Gly Ser Leu Ser Ser Asn Pro Ser

675

680

685

Ser Leu Thr Thr Ser Lys Glu Leu Ser Ser Ala Ser Asp Gly Tyr Ile
690 695 700

Phe Asn Pro Lys Asp Ile Val Glu Glu Thr Ala Thr Ala Tyr Ile Val
705 710 715 720

Arg His Gly Asp His Phe His Tyr Ile Pro Lys Ser Asn Gln Ile Gly
725 730 735

Gln Pro Thr Leu Pro Asn Asn Ser Leu Ala Thr Pro Ser Pro Ser Leu
740 745 750

Pro Ile Asn Pro Gly Thr Ser His Glu Lys His Glu Glu Asp Gly Tyr
755 760 765

Gly Phe Asp Ala Asn Arg Ile Ile Ala Glu Asp Glu Ser Gly Phe Val
770 775 780

Met Ser His Gly Asp His Asn His Tyr Phe Phe Lys Lys Asp Leu Thr
785 790 795 800

Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu Glu Val Lys Thr
805 810 815

Ser His Asn Gly Leu Asp Ser Leu Ser Ser His Glu Gln Asp Tyr Pro
820 825 830

Gly Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys Ile Glu Glu Lys
835 840 845

Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg Glu Ser Ile Val
850 855 860

Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro His Gly Asp His His
865 870 875 880

His Ala Asp Pro Ile Asp Glu His Lys Pro Val Gly Ile Gly His Ser
885 890 895

His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly Val Ala Lys Lys
900 905 910

Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr Asn Val Val Asn
915 920 925

Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe Thr Leu Ala Asn
930 935 940

Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro Glu Leu Glu Lys Lys
945 950 955 960

Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr Pro Asp Gly Lys Val
965 970 975

Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu Gly Val Gly Asn Ile
980 985 990

Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly Gln Thr Phe Lys
995 1000 1005

Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser Tyr Asp Gly
1010 1015 1020

Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala Ser Gln
1025 1030 1035

Thr Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg Val
1040 1045 1050

Asn Pro Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg
1055 1060 1065

Val Phe Asp Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr
1070 1075 1080

Lys Val Gly Glu Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly
1085 1090 1095

Thr Thr Arg Thr Ala Gly Asn Lys Ile Pro Val Thr Phe Met Ala
1100 1105 1110

Asn Ala Tyr Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu Val Pro
1115 1120 1125

Ile Leu Glu Lys Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu Pro
1130 1135 1140

Gln Phe Lys Arg Asn Lys Ala Gln Glu Asn Ser Lys Leu Asp Glu
1145 1150 1155

Lys Val Glu Glu Pro Lys Thr Ser Glu Lys Val Glu Lys Glu Lys
1160 1165 1170

Leu Ser Glu Thr Gly Asn Ser Thr Ser Asn Ser Thr Leu Glu Glu
1175 1180 1185

Val Pro Thr Val Asp Pro Val Gln Glu Lys Val Ala Lys Phe Ala
1190 1195 1200

Glu Ser Tyr Gly Met Lys Leu Glu Asn Val Leu Phe Asn Met Asp
1205 1210 1215

Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly Glu Val Ile Lys Lys
1220 1225 1230

Asn Met Ala Asp Phe Thr Gly Glu Ala Pro Gln Gly Asn Gly Glu
1235 1240 1245

Asn Lys Pro Ser Glu Asn Gly Lys Val Ser Thr Gly Thr Val Glu
1250 1255 1260

Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro Glu Ala
1265 1270 1275

Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn Gly
1280 1285 1290

Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu Asp
1295 1300 1305

Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu Lys
1310 1315 1320

Leu Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser Val
1325 1330 1335

Ile Phe Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser Gly
1340 1345 1350

Glu Val Ile Lys Lys Asn Leu Ser Asp Phe Ile Ala
1355 1360 1365

<210> 383
<211> 1126
<212> PRT
<213> Artificial Sequence

<220>
<223> Unknown Organism

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa = Methionine or nothing

<220>
<221> MISC_FEATURE
<222> (557)..(557)
<223> Xaa = Glycine or nothing

<220>
<221> MISC_FEATURE
<222> (558)..(558)
<223> Xaa = Proline or nothing

<400> 383

Xaa Asp Ile Asp Ser Leu Leu Lys Gln Leu Tyr Lys Leu Pro Leu Ser
1 5 10 15

Gln Arg His Val Glu Ser Asp Gly Leu Ile Phe Asp Pro Ala Gln Ile
20 25 30

Thr Ser Arg Thr Ala Arg Gly Val Ala Val Pro His Gly Asn His Tyr
35 40 45

His Phe Ile Pro Tyr Glu Gln Met Ser Glu Leu Glu Lys Arg Ile Ala
50 55 60

Arg Ile Ile Pro Leu Arg Tyr Arg Ser Asn His Trp Val Pro Asp Ser
65 70 75 80

Arg Pro Glu Glu Pro Ser Pro Gln Pro Thr Pro Glu Pro Ser Pro Ser

85

90

95

Pro Gln Pro Ala Pro Asn Pro Gln Pro Ala Pro Ser Asn Pro Ile Asp
 100 105 110

Glu Lys Leu Val Lys Glu Ala Val Arg Lys Val Gly Asp Gly Tyr Val
 115 120 125

Phe Glu Glu Asn Gly Val Ser Arg Tyr Ile Pro Ala Lys Asn Leu Ser
 130 135 140

Ala Glu Thr Ala Ala Gly Ile Asp Ser Lys Leu Ala Lys Gln Glu Ser
 145 150 155 160

Leu Ser His Lys Leu Gly Ala Lys Lys Thr Asp Leu Pro Ser Ser Asp
 165 170 175

Arg Glu Phe Tyr Asn Lys Ala Tyr Asp Leu Leu Ala Arg Ile His Gln
 180 185 190

Asp Leu Leu Asp Asn Lys Gly Arg Gln Val Asp Phe Glu Ala Leu Asp
 195 200 205

Asn Leu Leu Glu Arg Leu Lys Asp Val Ser Ser Asp Lys Val Lys Leu
 210 215 220

Val Asp Asp Ile Leu Ala Phe Leu Ala Pro Ile Arg His Pro Glu Arg
 225 230 235 240

Leu Gly Lys Pro Asn Ala Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln
 245 250 255

Val Ala Lys Leu Ala Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe
 260 265 270

Asp Pro Arg Asp Ile Thr Ser Asp Glu Gly Asp Ala Tyr Val Thr Pro
 275 280 285

His Met Thr His Ser His Trp Ile Lys Lys Asp Ser Leu Ser Glu Ala
 290 295 300

Glu Arg Ala Ala Ala Gln Ala Tyr Ala Lys Glu Lys Gly Leu Thr Pro
 305 310 315 320

Pro Ser Thr Asp His Gln Asp Ser Gly Asn Thr Glu Ala Lys Gly Ala
325 330 335

Glu Ala Ile Tyr Asn Arg Val Lys Ala Ala Lys Lys Val Pro Leu Asp
340 345 350

Arg Met Pro Tyr Asn Leu Gln Tyr Thr Val Glu Val Lys Asn Gly Ser
355 360 365

Leu Ile Ile Pro His Tyr Asp His Tyr His Asn Ile Lys Phe Glu Trp
370 375 380

Phe Asp Glu Gly Leu Tyr Glu Ala Pro Lys Gly Tyr Thr Leu Glu Asp
385 390 395 400

Leu Leu Ala Thr Val Lys Tyr Tyr Val Glu His Pro Asn Glu Arg Pro
405 410 415

His Ser Asp Asn Gly Phe Gly Asn Ala Ser Asp His Val Gln Arg Asn
420 425 430

Lys Asn Gly Gln Ala Asp Thr Asn Gln Thr Glu Lys Pro Ser Glu Glu
435 440 445

Lys Pro Gln Thr Glu Lys Pro Glu Glu Glu Thr Pro Arg Glu Glu Lys
450 455 460

Pro Gln Ser Glu Lys Pro Glu Ser Pro Lys Pro Thr Glu Glu Pro Glu
465 470 475 480

Glu Glu Ser Pro Glu Glu Ser Glu Glu Pro Gln Val Glu Thr Glu Lys
485 490 495

Val Glu Glu Lys Leu Arg Glu Ala Glu Asp Leu Leu Gly Lys Ile Gln
500 505 510

Asp Pro Ile Ile Lys Ser Asn Ala Lys Glu Thr Leu Thr Gly Leu Lys
515 520 525

Asn Asn Leu Leu Phe Gly Thr Gln Asp Asn Asn Thr Ile Met Ala Glu
530 535 540

Ala Glu Lys Leu Leu Ala Leu Leu Lys Glu Ser Lys Xaa Xaa Asp Leu
545 550 555 560

Thr Glu Glu Gln Ile Lys Ala Ala Gln Lys His Leu Glu Glu Val Lys
565 570 575

Thr Ser His Asn Gly Leu Asp Ser Leu Ser Ser His Glu Gln Asp Tyr
580 585 590

Pro Gly Asn Ala Lys Glu Met Lys Asp Leu Asp Lys Lys Ile Glu Glu
595 600 605

Lys Ile Ala Gly Ile Met Lys Gln Tyr Gly Val Lys Arg Glu Ser Ile
610 615 620

Val Val Asn Lys Glu Lys Asn Ala Ile Ile Tyr Pro His Gly Asp His
625 630 635 640

His His Ala Asp Pro Ile Asp Glu His Lys Pro Val Gly Ile Gly His
645 650 655

Ser His Ser Asn Tyr Glu Leu Phe Lys Pro Glu Glu Gly Val Ala Lys
660 665 670

Lys Glu Gly Asn Lys Val Tyr Thr Gly Glu Glu Leu Thr Asn Val Val
675 680 685

Asn Leu Leu Lys Asn Ser Thr Phe Asn Asn Gln Asn Phe Thr Leu Ala
690 695 700

Asn Gly Gln Lys Arg Val Ser Phe Ser Phe Pro Pro Glu Leu Glu Lys
705 710 715 720

Lys Leu Gly Ile Asn Met Leu Val Lys Leu Ile Thr Pro Asp Gly Lys
725 730 735

Val Leu Glu Lys Val Ser Gly Lys Val Phe Gly Glu Gly Val Gly Asn
740 745 750

Ile Ala Asn Phe Glu Leu Asp Gln Pro Tyr Leu Pro Gly Gln Thr Phe
755 760 765

Lys Tyr Thr Ile Ala Ser Lys Asp Tyr Pro Glu Val Ser Tyr Asp Gly
770 775 780

Thr Phe Thr Val Pro Thr Ser Leu Ala Tyr Lys Met Ala Ser Gln Thr
785 790 795 800

Ile Phe Tyr Pro Phe His Ala Gly Asp Thr Tyr Leu Arg Val Asn Pro
805 810 815

Gln Phe Ala Val Pro Lys Gly Thr Asp Ala Leu Val Arg Val Phe Asp
820 825 830

Glu Phe His Gly Asn Ala Tyr Leu Glu Asn Asn Tyr Lys Val Gly Glu
835 840 845

Ile Lys Leu Pro Ile Pro Lys Leu Asn Gln Gly Thr Thr Arg Thr Ala
850 855 860

Gly Asn Lys Ile Pro Val Thr Phe Met Ala Asn Ala Tyr Leu Asp Asn
865 870 875 880

Gln Ser Thr Tyr Ile Val Glu Val Pro Ile Leu Glu Lys Glu Asn Gln
885 890 895

Thr Asp Lys Pro Ser Ile Leu Pro Gln Phe Lys Arg Asn Lys Ala Gln
900 905 910

Glu Asn Ser Lys Leu Asp Glu Lys Val Glu Glu Pro Lys Thr Ser Glu
915 920 925

Lys Val Glu Lys Glu Lys Leu Ser Glu Thr Gly Asn Ser Thr Ser Asn
930 935 940

Ser Thr Leu Glu Glu Val Pro Thr Val Asp Pro Val Gln Glu Lys Val
945 950 955 960

Ala Lys Phe Ala Glu Ser Tyr Gly Met Lys Leu Glu Asn Val Leu Phe
965 970 975

Asn Met Asp Gly Thr Ile Glu Leu Tyr Leu Pro Ser Gly Glu Val Ile
980 985 990

Lys Lys Asn Met Ala Asp Phe Thr Gly Glu Ala Pro Gln Gly Asn Gly

995

1000

1005

Glu Asn Lys Pro Ser Glu Asn Gly Lys Val Ser Thr Gly Thr Val
 1010 1015 1020

Glu Asn Gln Pro Thr Glu Asn Lys Pro Ala Asp Ser Leu Pro Glu
 1025 1030 1035

Ala Pro Asn Glu Lys Pro Val Lys Pro Glu Asn Ser Thr Asp Asn
 1040 1045 1050

Gly Met Leu Asn Pro Glu Gly Asn Val Gly Ser Asp Pro Met Leu
 1055 1060 1065

Asp Pro Ala Leu Glu Glu Ala Pro Ala Val Asp Pro Val Gln Glu
 1070 1075 1080

Lys Leu Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly Leu Asp Ser
 1085 1090 1095

Val Ile Phe Asn Met Asp Gly Thr Ile Glu Leu Arg Leu Pro Ser
 1100 1105 1110

Gly Glu Val Ile Lys Lys Asn Leu Ser Asp Phe Ile Ala
 1115 1120 1125

<210> 384

<211> 913

<212> PRT

<213> Artificial Sequence

<220>

<223> Unknown Organism

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> Xaa = Methionine or nothing

<220>

<221> MISC_FEATURE

<222> (344)..(344)

<223> Xaa = Glycine or nothing

<220>

<221> MISC_FEATURE

<222> (345)..(345)
<223> Xaa = Proline or nothing

<400> 384

Xaa Asp Ile Leu Ala Phe Leu Ala Pro Ile Arg His Pro Glu Arg Leu
1 5 10 15

Gly Lys Pro Asn Ala Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val
20 25 30

Ala Lys Leu Ala Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp
35 40 45

Pro Arg Asp Ile Thr Ser Asp Glu Gly Asp Ala Tyr Val Thr Pro His
50 55 60

Met Thr His Ser His Trp Ile Lys Lys Asp Ser Leu Ser Glu Ala Glu
65 70 75 80

Arg Ala Ala Ala Gln Ala Tyr Ala Lys Glu Lys Gly Leu Thr Pro Pro
85 90 95

Ser Thr Asp His Gln Asp Ser Gly Asn Thr Glu Ala Lys Gly Ala Glu
100 105 110

Ala Ile Tyr Asn Arg Val Lys Ala Ala Lys Lys Val Pro Leu Asp Arg
115 120 125

Met Pro Tyr Asn Leu Gln Tyr Thr Val Glu Val Lys Asn Gly Ser Leu
130 135 140

Ile Ile Pro His Tyr Asp His Tyr His Asn Ile Lys Phe Glu Trp Phe
145 150 155 160

Asp Glu Gly Leu Tyr Glu Ala Pro Lys Gly Tyr Ser Leu Glu Asp Leu
165 170 175

Leu Ala Thr Val Lys Tyr Tyr Val Glu His Pro Asn Glu Arg Pro His
180 185 190

Ser Asp Asn Gly Phe Gly Asn Ala Ser Asp His Val Arg Lys Asn Lys
195 200 205

Ala Asp Gln Asp Ser Lys Pro Asp Glu Asp Lys Glu His Asp Glu Val
210 215 220

Ser Glu Pro Thr His Pro Glu Ser Asp Glu Lys Glu Asn His Ala Gly
225 230 235 240

Leu Asn Pro Ser Ala Asp Asn Leu Tyr Lys Pro Ser Thr Asp Thr Glu
245 250 255

Glu Thr Glu Glu Glu Ala Glu Asp Thr Thr Asp Glu Ala Glu Ile Pro
260 265 270

Gln Val Glu Asn Ser Val Ile Asn Ala Lys Ile Ala Asp Ala Glu Ala
275 280 285

Leu Leu Glu Lys Val Thr Asp Pro Ser Ile Arg Gln Asn Ala Met Glu
290 295 300

Thr Leu Thr Gly Leu Lys Ser Ser Leu Leu Leu Gly Thr Lys Asp Asn
305 310 315 320

Asn Thr Ile Ser Ala Glu Val Asp Ser Leu Leu Ala Leu Leu Lys Glu
325 330 335

Ser Gln Pro Ala Pro Ile Gln Xaa Xaa Asp Leu Thr Glu Glu Gln Ile
340 345 350

Lys Ala Ala Gln Lys His Leu Glu Glu Val Lys Thr Ser His Asn Gly
355 360 365

Leu Asp Ser Leu Ser Ser His Glu Gln Asp Tyr Pro Gly Asn Ala Lys
370 375 380

Glu Met Lys Asp Leu Asp Lys Lys Ile Glu Glu Lys Ile Ala Gly Ile
385 390 395 400

Met Lys Gln Tyr Gly Val Lys Arg Glu Ser Ile Val Val Asn Lys Glu
405 410 415

Lys Asn Ala Ile Ile Tyr Pro His Gly Asp His His His Ala Asp Pro
420 425 430

Ile Asp Glu His Lys Pro Val Gly Ile Gly His Ser His Ser Asn Tyr
435 440 445

Glu Leu Phe Lys Pro Glu Glu Gly Val Ala Lys Lys Glu Gly Asn Lys
450 455 460

Val Tyr Thr Gly Glu Glu Leu Thr Asn Val Val Asn Leu Leu Lys Asn
465 470 475 480

Ser Thr Phe Asn Asn Gln Asn Phe Thr Leu Ala Asn Gly Gln Lys Arg
485 490 495

Val Ser Phe Ser Phe Pro Pro Glu Leu Glu Lys Lys Leu Gly Ile Asn
500 505 510

Met Leu Val Lys Leu Ile Thr Pro Asp Gly Lys Val Leu Glu Lys Val
515 520 525

Ser Gly Lys Val Phe Gly Glu Gly Val Gly Asn Ile Ala Asn Phe Glu
530 535 540

Leu Asp Gln Pro Tyr Leu Pro Gly Gln Thr Phe Lys Tyr Thr Ile Ala
545 550 555 560

Ser Lys Asp Tyr Pro Glu Val Ser Tyr Asp Gly Thr Phe Thr Val Pro
565 570 575

Thr Ser Leu Ala Tyr Lys Met Ala Ser Gln Thr Ile Phe Tyr Pro Phe
580 585 590

His Ala Gly Asp Thr Tyr Leu Arg Val Asn Pro Gln Phe Ala Val Pro
595 600 605

Lys Gly Thr Asp Ala Leu Val Arg Val Phe Asp Glu Phe His Gly Asn
610 615 620

Ala Tyr Leu Glu Asn Asn Tyr Lys Val Gly Glu Ile Lys Leu Pro Ile
625 630 635 640

Pro Lys Leu Asn Gln Gly Thr Thr Arg Thr Ala Gly Asn Lys Ile Pro
645 650 655

Val Thr Phe Met Ala Asn Ala Tyr Leu Asp Asn Gln Ser Thr Tyr Ile

660

665

670

Val Glu Val Pro Ile Leu Glu Lys Glu Asn Gln Thr Asp Lys Pro Ser
 675 680 685

Ile Leu Pro Gln Phe Lys Arg Asn Lys Ala Gln Glu Asn Ser Lys Leu
 690 695 700

Asp Glu Lys Val Glu Glu Pro Lys Thr Ser Glu Lys Val Glu Lys Glu
 705 710 715 720

Lys Leu Ser Glu Thr Gly Asn Ser Thr Ser Asn Ser Thr Leu Glu Glu
 725 730 735

Val Pro Thr Val Asp Pro Val Gln Glu Lys Val Ala Lys Phe Ala Glu
 740 745 750

Ser Tyr Gly Met Lys Leu Glu Asn Val Leu Phe Asn Met Asp Gly Thr
 755 760 765

Ile Glu Leu Tyr Leu Pro Ser Gly Glu Val Ile Lys Lys Asn Met Ala
 770 775 780

Asp Phe Thr Gly Glu Ala Pro Gln Gly Asn Gly Glu Asn Lys Pro Ser
 785 790 795 800

Glu Asn Gly Lys Val Ser Thr Gly Thr Val Glu Asn Gln Pro Thr Glu
 805 810 815

Asn Lys Pro Ala Asp Ser Leu Pro Glu Ala Pro Asn Glu Lys Pro Val
 820 825 830

Lys Pro Glu Asn Ser Thr Asp Asn Gly Met Leu Asn Pro Glu Gly Asn
 835 840 845

Val Gly Ser Asp Pro Met Leu Asp Pro Ala Leu Glu Glu Ala Pro Ala
 850 855 860

Val Asp Pro Val Gln Glu Lys Leu Glu Lys Phe Thr Ala Ser Tyr Gly
 865 870 875 880

Leu Gly Leu Asp Ser Val Ile Phe Asn Met Asp Gly Thr Ile Glu Leu
 885 890 895

Arg Leu Pro Ser Gly Glu Val Ile Lys Lys Asn Leu Ser Asp Phe Ile
900 905 910

Ala